

FORM PTO-1390
(REV. 9-95)

U.S. DEPARTMENT OF COMMERCE, PATENT AND TRADEMARK OFFICE

ATTORNEY'S DOCKET NUMBER

**TRANSMITTAL LETTER TO THE UNITED STATES
DESIGNATED/ELECTED OFFICE (DO/EO/US)
CONCERNING A FILING UNDER 35 U.S.C. §371**

SCH 1761

U.S. APPLICATION NO. (If known, see 37 CFR §1.5)

09/623746

INTERNATIONAL APPLICATION NO.

INTERNATIONAL FILING DATE

PCT/DE99/00722

9 MARCH 1999

PRIORITY DATE CLAIMED

10 MARCH 1998

TITLE OF INVENTION

HUMAN NUCLEIC ACID SEQUENCES FROM PROSTATE TISSUE

APPLICANT(S) FOR DO/EO/US

SPEC'Ht, Thomas, et al.



Applicant herewith submits to the United States Designated/Elected Office (DO/EO/US) the following items and other information:

1. ☒ This is a **FIRST** submission of items concerning a filing under 35 U.S.C. §371.
 2. ☐ This is a **SECOND** or **SUBSEQUENT** submission of items concerning a filing under 35 U.S.C. §371.
 3. ☐ This express request to begin national examination procedures (35 U.S.C. §371(f)) at any time rather than delay examination until the expiration of the applicable time limit set in 35 U.S.C. §371(b) and PCT Articles 22 and 39(1).
 4. ☒ A proper Demand for International Preliminary Examination was made by the 19th month from the earliest claimed priority date.
 5. ☒ A copy of the International Application as filed (35 U.S.C. §371(c)(2))
 - a. ☐ is transmitted herewith (required only if not transmitted by the International Bureau).
 - b. ☒ has been transmitted by the International Bureau.
 - c. ☐ is not required, as the application was filed in the United States Receiving Office (RO/US)
 6. ☒ A translation of the International Application into English (35 U.S.C. §371(c)(2)).
 7. ☒ Amendments to the claims of the International Application under PCT Article 19 (35 U.S.C. §371(c)(3))
 - a. ☐ are transmitted herewith (required only if not transmitted by the International Bureau).
 - b. ☐ have been transmitted by the International Bureau.
 - c. ☐ have not been made; however, the time limit for making such amendments has NOT expired.
 - d. ☒ have not been made and will not be made.
 8. ☐ A translation of the amendments to the claims under PCT Article 19 (35 U.S.C. §371(c)(3)).
 9. ☐ An oath or declaration of the inventor(s) (35 U.S.C. §371(c)(4)).
 10. ☐ A translation of the annexes to the International Preliminary Examination Report under PCT Article 36 (35 U.S.C. §371(c)(5))
- Items 11. to 16. below concern document(s) or information included:**
11. ☐ An Information Disclosure Statement under 37 C.F.R. §§1.97 and 1.98.
 12. ☐ An assignment document for recording. A separate cover sheet in compliance with 37 C.F.R. §§3.28 and 3.31 is included.
 13. ☒ A FIRST preliminary amendment.
 - ☐ A SECOND or SUBSEQUENT preliminary amendment.
 14. ☐ A substitute specification.
 15. ☐ A change of power of attorney and/or address letter.
 16. ☒ Other items or information: PAPER AND DISKETTE COPY OF SEQUENCE LISTING

U.S. APPLICATION NO. (if known, see 37 CFR §1.5)

INTERNATIONAL APPLICATION NO.

ATTORNEY'S DOCKET NUMBER

09/623746

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SCH 1761

- 17.
- ☒
- The following fees are submitted:

BASIC NATIONAL FEE (37 CFR §1.492 (a) (1) - (5)):

Search Report has been prepared by the EPO or JPO..... \$840.00
 International preliminary examination fee paid to USPTO (37 CFR §1.482)..... \$670.00
 No international preliminary examination fee paid to USPTO (37 CFR §1.482) but international search fee paid to USPTO (37 CFR §1.445(a)(2))..... \$760.00
 Neither international preliminary examination fee (37 CFR §1.482) nor international search fee (37 CFR §1.445(a)(2)) paid to USPTO..... \$970.00
 International preliminary examination fee paid to USPTO (37 CFR §1.482) and all claims satisfied provisions of PCT Article 33(2)-(4)..... \$96.00

CALCULATIONS PTO USE ONLY**ENTER APPROPRIATE BASIC FEE AMOUNT =****\$840.00**

Surcharge of **\$130.00** for furnishing the oath or declaration later than months from the earliest claimed priority date (37 C.F.R. §1.492(e)). ☐ 20 ☐ 30

CLAIMS	NUMBER FILED	NUMBER EXTRA	RATE	
Total claims	37 - 20 =	17	x \$ 18.00	\$306.00
Independent claims	5 - 3 =	2	x \$ 78.00	\$156.00
MULTIPLE DEPENDENT CLAIM(S) (if applicable)			+ \$ 260.00	

TOTAL OF ABOVE CALCULATIONS =**\$1,302.00**

Reduction of 1/2 for filing by small entity, if applicable. A Verified Small Entity Statement must also be filed (Note 37 C.F.R. §§1.9, 1.27, 1.28).

SUBTOTAL =**\$1,302.00**

Processing fee of **\$130.00** for furnishing the English translation later than months from the earliest claimed priority date (37 C.F.R. §1.492(f)). ☐ 20 ☐ 30

TOTAL NATIONAL FEE =**\$1,302.00**

Fee for recording the enclosed assignment (37 C.F.R. §1.21(h)). The assignment must be accompanied by an appropriate cover sheet (37 C.F.R. §§3.28, 3.31). \$40.00 per property.

TOTAL FEES ENCLOSED =**\$1,302.00**

Amount to be refunded:
charged:

- a. ☒ A check in the amount of **\$1,302.00** to cover the above fees is enclosed
- b. ☐ Please charge my Deposit Account No. **13-3402** in the amount of \$_____ to cover the above fees. A duplicate copy of this sheet is enclosed.
- c. ☒ The Commissioner is hereby authorized to charge any additional fees which may be required, or credit any overpayment to Deposit Account No. **13-3402**. A duplicate copy of this sheet is enclosed

NOTE: Where an appropriate time limit under 37 C.F.R. §§1.494 or 1.495 has not been met, a petition to revive (37 C.F.R. §1.137(a) or (b)) must be filed and granted to restore the application to pending status.

SEND ALL CORRESPONDENCE TO.

MILLEN, WHITE, ZELANO & BRANIGAN, P.C.
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Filed: 8 SEPTEMBER 2000

AJZ:jmm

SIGNATURE

Anthony J. Zelano

NAME

27,969

REGISTRATION NUMBER

IN THE UNITED STATES DESIGNATED/ELECTED OFFICE (DO/EO/US)

International Application No. : PCT/DE99/00722
 International Filing Date : 9 MARCH 1999
 U.S. Serial No. : 09/623,746
 Deposit Date U.S. Nat'l Phase : 8 SEPTEMBER 2000
 Priority Date(s) Claimed : 10 MARCH 1998
 Applicant(s) : SPECHT, Thomas, et al.
 Title: HUMAN NUCLEIC ACID SEQUENCES FROM PROSTATE TISSUE



RESPONSE TO NOTIFICATION OF MISSING REQUIREMENTS
UNDER 35 U.S.C. § 371
IN THE UNITED STATES DESIGNATED/ELECTED OFFICE (DO/EO/US)

Commissioner for Patents
 Box PCT
 Washington, D.C. 20231

Sir:

In response to the Notification of Missing Requirements mailed October 27, 2000, attached is a Declaration and Power of Attorney for Patent Application which has been executed by the inventors, as well as a copy of the Notification.

The Surcharge of \$130.00 for providing the Declaration later than 30 months from the original priority date is attached.

Applicants request that the time for responding to this action be extended one (1) month to December 27, 2000. A check for the statutory fee of \$110 is enclosed.

Also enclosed are ten (10) sheets of drawings, properly translated.

12/29/2000 UEDUVIJE 00000017 09623746

01 FC:154	130.00 DP
02 FC:115	110.00 DP

IN THE UNITED STATES DESIGNATED/ELECTED OFFICE

International Application No. : PCT/DE99/00722
 International Filing Date : 9 MARCH 1999
 Priority Date(s) Claimed : 10 MARCH 1998
 Applicant(s) (DO/EO/US) : SPECHT, Thomas, et al.

Title: HUMAN NUCLEIC ACID SEQUENCES FROM PROSTATE TISSUE

PRELIMINARY AMENDMENT

Commissioner for Patents
 Washington, D.C. 20231

SIR:

Prior to calculating the national fee, and prior to examination in the National Phase of the above-identified International application, please amend as follows:

IN THE CLAIMS:

- Claim 5, line 1, delete "claims 1 to 4" and insert --Claim 3--;
- Claim 6, line 1, delete "claims 1 to 4" and insert --Claim 3--;
- Claim 7, line 2, delete "claims 1 to 6" and insert --Claim 3--;
- line 4, delete "claims 1 to 6" and insert --Claim 3--;
- Claim 8, line 1, delete "claims 1 to 7" and insert --Claim 3--;
- Claim 9, line 1, delete "claims 1 to 7" and insert --Claim 3--;
- Claim 10, lines 1 and 2, delete "claims 1 to 9" and insert --Claim 3--;
- Claim 11, line 2, delete "one of claims 1 to 9" and insert --Claim 3--;
- Claim 13, lines 1 and 2, delete "one of claims 11 and 12" and insert --Claim 11--;
- Claim 14, lines 1 and 2, delete "claims 1 to 10" and insert --Claim 3--;
- Claim 16, line 3, delete "one of claims 1 to 10" and insert --Claim 3--;
- Claim 18, line 1, delete "one of claims 16 or 17" and insert --Claim 16--;
- Claim 19, line 2, delete "claims 16 to 18" and insert --Claim 16--;
- Claim 26, line 1, after "partial sequences" insert --of Claim 23--;
- Claim 27, line 1, after "acid sequences" insert --of Claim 2--;
- Claim 28, line 1, after "acid sequences" insert --of Claim 2--;

Claim 29, line 1, after "partial sequences" insert --of Claim 23--;
Claim 30, line 1, after "partial sequences" insert --of Claim 23--;
Claim 31, line 2, after "partial sequence" insert --of Claim 23--;
Claim 32, line 1, delete "claims 1 to 10" and insert --Claim 3--;
Claim 33, line 1, delete "claims 1 to 10" and insert --Claim 3--;
Claim 34, line 3, after "sequences" insert --of Claim 2--;
Claim 37, line 1, delete "claims 1 to 7" and insert --Claim 3--.

REMARKS

The purpose of this Preliminary Amendment is to eliminate multiple dependent claims in order to avoid the additional fee. Applicants reserve the right to reintroduce claims to canceled combined subject matter.

Respectfully submitted,



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AJZ:jmm

Human Nucleic Acid Sequences from Prostate Tissue

The invention relates to human nucleic acid sequences -- mRNA, cDNA, genomic sequences -- from normal prostate tissue, which code for gene products or parts thereof and their use.

The invention furthermore relates to polypeptides that can be obtained via the sequences and their use.

One very common type of cancer is prostate cancer, for control of which new therapies are necessary. Previously used therapies that are based on a blocking of hormone effects are very often ineffective after a few years since the tumor becomes independent of the hormone, i.e., it continues to grow and forms metastases without the action of hormones.

The cancer phenomenon often goes along with overexpression or underexpression of certain genes in degenerated cells, it still being unclear whether these altered expression rates are the cause or the result of the malignant transformation. Identification of these genes would be an important step for development of new therapies against cancer. Spontaneous formation of cancer is often preceded by a host of mutations. They can have the most varied effects on the expression pattern in the affected tissue, such as, e.g., underexpression or overexpression, but also expression of shortened genes. Several such changes due to these mutation cascades can ultimately lead to malignant degeneration. The complexity of these relationships makes an experimental approach very difficult.

A database which consists of so-called ESTs is used to look for candidate genes, i.e., genes that compared to the tumor tissue are more strongly expressed in normal tissue.

ESTs (expressed sequence tags) are sequences of cDNAs, i.e., mRNAs transcribed in reverse, therefore molecules that reflect gene expression. The EST sequences are determined for normal and degenerated tissue. These databases are offered to some extent commercially by various companies. The ESTs of the LifeSeq database, which is used here, are generally between 150 and 350 nucleotides long. They represent a pattern that is unmistakable for a certain gene, although this gene is normally very much longer (> 2000 nucleotides). By comparison of the expression patterns of normal and tumor tissue, ESTs can be identified which are important for tumor formation and proliferation (see Figure 1).

There is, however, the following problem: Since the EST sequences found can belong to different regions of an unknown gene due to different constructions of cDNA libraries, in this case a completely incorrect ratio of the occurrence of these ESTs in the respective tissue would arise. This would only be noticed when the complete gene is known and thus ESTs can be assigned to the same gene.

It has now been found that this error possibility can be reduced if all ESTs from the respective tissue type are assembled beforehand, before the expression patterns are compared to one another. Therefore overlapping ESTs of the same gene were combined into longer sequences (see Figure 1, Figure 2a and Fig.

3). This lengthening and thus coverage of an essentially larger gene area in each of the respective bases are intended to largely avoid the above described error. Since there were no existing software products for this purpose, programs for assembling genomic sections were employed which were used modified and to which our own programs were added. A flow chart of the assembly procedure is shown in Figures 2b1 - 2b4.

Nucleic acid sequences Seq. ID No. 2-4, 6-10, 12-14, 16-19, 21, 23, 24, 26-33, 35-37, 39, 41-44, 46, 47, 49, 51-55, 58-64 and Seq. ID No. 217-247 which play a part as candidate genes in prostate cancer have now been found.

Nucleic acid sequences Seq. ID No. 3, 4, 6-8, 12, 16-19, 21, 23, 24, 26-33, 35, 37, 41-44, 46, 47, 49, 51, 53, 54, 58-64 and 217-247 are of special interest.

The invention thus relates to nucleic acid sequences, which code a gene product or a part thereof, comprising

- a) a nucleic acid sequence selected from the group of nucleic acid sequences Seq. ID No. 3, 4, 6-8, 12, 16-35, 37, 41-44, 46, 47, 49, 51, 53, 54, 58-64 and 217-247,
 - b) an allelic variation of the nucleic acid sequences named under a)
- or
- c) a nucleic acid sequence which is complementary to the nucleic acid sequences named under a) or b).

The invention furthermore relates to a nucleic acid sequence according to one of the sequences Seq. ID No. 3, 4, 6-8, 12, 16-

19, 21, 23, 24, 26-33, 35, 37, 41-44, 46, 47, 49, 51, 53, 54, 58-64 and 217-247 or a complementary or allelic variant thereof and the nucleic acid sequences thereof, which have 90% to 95% homology to a human nucleic acid sequence.

The invention also relates to nucleic acid sequences Seq. ID No. 2-4, 6-10, 12-14, 16-19, 21, 23, 24, 26-33, 35-37, 39, 41-44, 46, 47, 49, 51-55, 58-64 and 217-247, which are expressed elevated in the normal prostate tissue.

The invention furthermore relates to nucleic acid sequences comprising part of the aforementioned nucleic acid sequences in such a sufficient amount that they hybridize with sequences Seq. ID No. 3, 4, 6-8, 12, 16-19, 21, 23, 24, 26-33, 35, 37, 41-44, 46, 47, 49, 51, 53, 54, 58-64 and 217-247.

The nucleic acid sequences according to the invention generally have a length of at least 50 to 2500 bp, preferably a length of at least 150 to 2000 bp, especially a length from 400 to 1900 bp.

With the partial sequences Seq. ID No. 3, 4, 6-8, 12, 16-19, 21, 23, 24, 26-33, 35, 37, 41-44, 46, 47, 49, 51, 53, 54, 58-64 and 217-247 according to the invention, expression cassettes can also be built using current process practice, whereby on the cassette at least one of the nucleic acid sequences according to the invention is combined with at least one control or regulatory sequence generally known to one skilled in the art, such as, e.g., a suitable promoter. The sequences according to the invention can be inserted in a sense or antisense orientation.

A large number of expression cassettes or vectors and promoters which can be used are known in the literature.

Expression cassettes and vectors are defined as:

1. bacterial, such as, e.g., phagescript, pBs, ϕ X174, pBluescript SK, pBs KS, pNH8a, pNH16a, pNH18a, pNH46a (Stratagene), pTrc99A, pKK223-3, pKK233-3, pDR540, pRIT5 (Pharmacia), 2. eukaryotic, such as, e.g., pWLneo, pSV2cat, pOG44, pXT1, pSG (Stratagene), pSVK3, pBPV, pMSG, pSVL (Pharmacia).

A control or regulatory sequence is defined as suitable promoters. Here, two preferred vectors are the pKK232-8 and the PCM7 vector. In particular, the following promoters are intended: lacI, lacZ, T3, T7, gpt, lambda P_R, trc, CMV, HSV thymidine-kinase, SV40, LTRs from retrovirus and mouse metallothionein-I.

The DNA sequences located on the expression cassette can code a fusion protein which comprises a known protein and a bioactive polypeptide fragment.

The expression cassettes are likewise the subject matter of this invention.

The nucleic acid fragments according to the invention can be used to produce full-length genes. The obtainable genes are likewise the subject matter of this invention.

The invention also relates to the use of the nucleic acid sequences according to the invention and the gene fragments obtainable from use.

The nucleic acid sequences according to the invention can be moved into host cells with suitable vectors, in which as the

heterologous part, the genetic information which is contained on the nucleic acid fragments and which is expressed is located.

The host cells containing the nucleic acid fragments are likewise the subject matter of this invention.

Suitable host cells are, e.g., prokaryotic cell systems such as E. coli or eukaryotic cell systems such as animal or human cells or yeasts.

The nucleic acid sequences according to the invention can be used in the sense or antisense form.

Production of polypeptides or their fragments is done by cultivation of the host cells according to current cultivation methods and subsequent isolation and purification of the peptides or fragments, likewise using current methods. The invention furthermore relates to nucleic acid sequences, which code at least a partial sequence of a bioactive polypeptide.

Furthermore, this invention relates to polypeptide partial sequences, so-called ORF (open-reading-frame) peptides according to the sequence protocols Seq. ID No. 66-71, 73-75, 82, 83, 90-93, 97-105, 109, 111-114, 116-124, 128-137, 139-149, 152, 154-165, 168-173, 183-195, 214-216 and up to Seq. ID No. 248-295.

The invention furthermore relates to polypeptide sequences that have at least 80% homology, especially 90% homology to the polypeptide partial sequences of Seq. ID No. 66-71, 73-75, 82, 83, 90-93, 97-105, 109, 111-114, 116-124, 128-137, 139-149, 152, 154-165, 168-173, 183-195, 214-216 and up to Seq. ID No. 248-295 according to the invention.

The invention also relates to antibodies that are directed against a polypeptide or a fragment and that are coded by the nucleic acids of sequences Seq. ID No. 66-71, 73-75, 82, 83, 90-93, 97-105, 109, 111-114, 116-124, 128-137, 139-149, 152, 154-165, 168-173, 183-195, 214-216 and up to Seq. ID No. 248-295 according to the invention.

Antibodies are defined especially as monoclonal antibodies.

The invention also relates to phage display proteins, which are directed against a polypeptide or a fragment, and which are coded by the nucleic acids of sequences Seq. ID No. 66-71, 73-75, 82, 83, 90-93, 97-105, 109, 111-114, 116-124, 128-137, 139-149, 152, 154-165, 168-173, 183-195, 214-216 and up to Seq. ID No. 248-295 according to the invention.

The polypeptides of sequences Seq. ID No. 66-71, 73-75, 82, 83, 90-93, 97-105, 109, 111-114, 116-124, 128-137, 139-149, 152, 154-165, 168-173, 183-195, 214-216 and up to Seq. ID No. 248-295 according to the invention can also be used as tools for finding active agents against prostate cancer; this is likewise the subject matter of this invention.

Likewise the subject matter of this invention is the use of nucleic acid sequences according to sequences Seq. ID No. 66-71, 73-75, 82, 83, 90-93, 97-105, 109, 111-114, 116-124, 128-137, 139-149, 152, 154-165, 168-173, 183-195, 214-216 and up to Seq. ID No. 248-295 for expression of polypeptides, which can also be used as tools for finding active agents against prostate cancer.

The invention also relates to the use of the found polypeptide partial sequences Seq. ID No. 66-71, 73-75, 82, 83,

90-93, 97-105, 109, 111-114, 116-124, 128-137, 139-149, 152, 154-165, 168-173, 183-195, 214-216 and up to Seq. ID No. 248-295 as pharmaceutical agents in gene therapy for treatment of prostate cancer, or to produce a pharmaceutical agent for treatment of prostate cancer.

The invention also relates to pharmaceutical agents that contain at least one polypeptide partial sequence Seq. ID No. 66-71, 73-75, 82, 83, 90-93, 97-105, 109, 111-114, 116-124, 128-137, 139-149, 152, 154-165, 168-173, 183-195, 214-216 and up to Seq. ID No. 248-295.

The nucleic acid sequences found according to the invention can also be genomic or mRNA sequences.

The invention also relates to genomic genes, their promoters, enhancers, silencers, exon structure, intron structure and their splice versions, obtainable from cDNAs of sequences Seq. ID No. 3, 4, 6-8, 12, 16-19, 21, 23, 24, 26-33, 35, 37, 41-44, 46, 47, 49, 51, 53, 54, 58-64 and 217-247 and their use together with suitable regulatory elements, such as suitable promoters and/or enhancers.

With the nucleic acids according to the invention (cDNA sequences), genomic BAC, PAC and Cosmid libraries are screened and specifically human clones are isolated via complementary base pairing (hybridization). The BAC, PAC and Cosmid clones isolated in this way are hybridized using fluorescence-in-situ hybridization on metaphase chromosomes and the corresponding chromosome sections on which the corresponding genomic genes lie are identified. BAC, PAC and Cosmid clones are sequenced in

order to clarify the corresponding genomic genes in their complete structure (promoters, enhancers, silencers, exons and introns). BAC, PAC and Cosmid clones can be used as independent molecules for gene transfer (see Figure 5).

The invention also relates to BAC, PAC and Cosmid clones containing functional genes and their chromosomal localization according to sequences Seq. ID No. 3, 4, 6-8, 12, 16-19, 21, 23, 24, 26-33, 35, 37, 41-44, 46, 47, 49, 51, 53, 54, 58-64 and 217-247 for use as vehicles for gene transfer.

Meanings of technical terms and abbreviations

Nucleic acids= Nucleic acids in this invention are defined as:

mRNA, partial cDNA, full-length cDNA and genomic genes (chromosomes).

ORF = Open Reading Frame, a defined sequence of amino acids which can be derived from the cDNA sequence.

Contig = A set of DNA sequences which can be combined as a result of very great similarities into one sequence (consensus).

Singleton = A contig that contains only one sequence.

Module = Domain of a protein with a defined sequence, which represents one structural unit and which occurs in different proteins.

N = selectively the nucleotide A, T, G or C.

X = selectively one of the 20 naturally occurring amino acids.

Explanation of the alignment parameters

minimal initial match = minimal initial identity area
 maximum pads per read = maximum number of insertions
 maximum percent mismatch = maximum deviation in %

Explanation of Figures

Figure 1 shows the systematic gene search in the
 Incyte LifeSeq database.

Figure 2 shows the principle of EST assembling

Figures 2b1-2b4 show the entire principle of EST assembling

Figure 3 shows the in-silico subtraction of gene
 expression in different tissues

Figure 4a shows the determination of tissue-specific
 expression via electronic Northern

Figure 4b shows the electronic Northern

Figure 5 shows the isolation of genomic BAC and PAC
 clones.

The following examples explain the production of the nucleic acid sequences according to the invention without limiting the invention to these examples and nucleic acid sequences.

Example 1

Search for tumor-related candidate genes

First, all ESTs of the corresponding tissue from the LifeSeq database (from October 1997) were extracted. They were then assembled by means of the GAP4 program of the Staden package with the parameters 0% mismatch, 8 pads per read and a minimal match of 20. The sequences (fails) not recorded in the GAP4 database were assembled first at 1% mismatch and then again at 2% mismatch with the database. Consensus sequences were computed from the contigs of the database that consisted of more than one sequence (see Figures 2a and 2b1-2b4).

The singletons of the database, which consisted of only one sequence, were re-assembled at 2% mismatch with the sequences not recorded in the GAP4 database. In turn, the consensus sequences were determined for the contigs. All other ESTs were re-assembled at 4% mismatch. The consensus sequences were extracted once again and finally assembled with the previous consensus sequences and the singletons and the sequences not recorded in the database at 4% mismatch. The consensus sequences were formed and used with the singletons and fails as the initial basis for tissue comparisons. This procedure ensured that among the parameters used, all sequences represented gene regions independent of one another.

Figures 2b1-2b4 illustrate the lengthening of the normal prostate tissue ESTs.

The sequences of the respective tissue assembled in this way were then compared to one another by means of the same program (see Figure 3). To do this, first all sequences of the first tissue were input into the database. (It was therefore important that they were independent of one another).

Then, all sequences of the second tissue were compared to all those of the first. The result was sequences that were specific to the first or the second tissue as well as those which occurred in both. In the latter, the ratio of the frequency of occurrence in the respective tissue was evaluated.

All sequences that occurred more than four times in one of the compared tissues and all that occurred at least five times as often in one of the two tissues were further studied. These sequences were subjected to an electronic Northern (see Example 2.1), by which the distribution in all tumor and normal tissues was studied (see Figure 4a and Figure 4b). The relevant candidates were then lengthened using all Incyte ESTs and all ESTs of public databases (see Example 3). Then, the sequences and their translation into possible proteins were compared to all nucleotide and protein databases and were studied for possible regions that code for proteins.

Example 2**Algorithm for identification and lengthening of partial cDNA sequences with altered expression pattern**

An algorithm for finding overexpressed or underexpressed genes will be explained below. The individual steps are also summarized in a flow chart for the sake of clarity (see Figure 4b).

2.1. Electronic Northern Blot

By means of a standard program for homology search, e.g., BLAST (Altschul, S. F.; Gish, W.; Miller, W.; Myers, E.W. and Lipman, D.J. (1990) J. Mol. Biol. 215, 403-410), BLAST2 (Altschul, S. F.; Madden, T.L.; Schaeffer, A.A.; Zhang, J.; Zhang, Z.; Miller, W., and Lipman, D.J. (1997) Nucleic Acids Research 25 3389-3402) or FASTA (Pearson, W.R. and Lipman, D.J. (1988) Proc. Natl. Acad. Sci. USA 85 2444-2448), the homologous sequences in different EST libraries (private or public) arranged by tissues are determined for a partial DNA sequence S, e.g., an individual EST or a contig of ESTs. The (relative or absolute) tissue-specific occurrence frequencies of this partial sequence S which were determined in this way are called electronic Northern Blot.

2.1.1

Analogously to the procedure described under 2.1, the sequence Seq. ID No. 10 was found which occurs 4x more heavily in normal prostate tissue than in the corresponding tumor tissue.

The possible function of this gene region relates to human MVF-1.

The result is as follows:

Electronic Northern Blot for Seq. ID No.: 10

	NORMAL % freq.	TUMOR % freq.	Ratios N/T T/N	
	0.0000	0.0026	0.0000	undef
Bladder	0.0040	0.0022	1.8347	0.5450
Breast	0.0061	0.0052	1.1686	0.8557
Ovary	0.0055	0.0000	undef	0.0000
Endocrine tissue	0.0039	0.0000	undef	0.0000
Gastrointestinal	0.0017	0.0088	0.1935	5.1673
Brain	0.0014	0.0000	undef	0.0000
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0065	0.0000	undef
Hepatic	0.0021	0.0000	undef	0.0000
Heart	0.0000	0.0000	undef	undef
Testicles	0.0050	0.0024	2.1069	0.4746
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0051	0.0000	undef	undef
Muscle-skeleton	0.0030	0.0068	0.4342	2.3033
Kidney	0.0019	0.0000	undef	0.0000
Pancreas	0.0030	0.0000	undef	0.0000
Penis	0.0095	0.0021	4.4745	0.2235
Prostate	0.0017	0.0071	0.2321	4.3088
Uterus	0.0145			
Breast hyperplasia	0.0000			
Small intestine	0.0149			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0026			

	FETUS % freq.
Development	0.0000
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0000
Heart-blood vessels	0.0041
Lung	0.0111
Kidney	0.0124
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES % frequency

Breast	0.0000
Ovary-uterus	0.0000
Endocrine tissue	0.0000
Fetal	0.0082
Gastrointestinal	0.0244
Hematopoietic	0.0114
Skin-muscle	0.0000
Testicles	0.0000
Lung	0.0000
Nerves	0.0040
Prostate	0.0128
Sensory organs	0.0000

2.1.2

Analogously to the procedure described under 2.1, the sequence Seq. ID No. 18 was found which occurs 6x more heavily in normal prostate tissue than in the tumor tissue.

The result is as follows:

Electronic Northern Blot for Seq. ID No.: 18

	NORMAL % freq.	TUMOR % freq.	Ratios N/T T/N	
	0.0279	0.0026	10.9109	0.0917
Bladder	0.0040	0.0022	1.8347	0.5450
Breast	0.0000	0.0026	0.0000	undef
Ovary	0.0018	0.0000	undef	0.0000
Endocrine tissue	0.0116	0.0000	undef	0.0000
Gastrointestinal	0.0042	0.0033	1.2902	0.7751
Brain	0.0014	0.0000	undef	0.0000
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0065	0.0000	undef
Hepatic	0.0021	0.0000	undef	0.0000
Heart	0.0000	0.0000	undef	undef
Testicles	0.0037	0.0000	undef	0.0000
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0034	0.0000	undef	0.0000
Muscle-skeleton	0.0089	0.0000	undef	0.0000
Kidney	0.0019	0.0055	0.3428	2.9168
Pancreas	0.0060	0.0000	undef	0.0000
Penis	0.0119	0.0021	5.5932	0.1788
Prostate	0.0033	0.0071	0.4642	2.1544
Uterus	0.0000			
Breast hyperplasia	0.0000			
Small intestine	0.0000			
Prostate hyperplasia	0.0030			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0017			

FETUS % freq.

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0000
Heart-blood vessels	0.0039
Lung	0.0000
Kidney	0.0000
Prostate	0.0124
Sensory organs	0.0000
	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES % frequency

Breast	0.0272
Ovary-uterus	0.0000
Endocrine tissue	0.0000
Fetal	0.0012
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0065
Testicles	0.0000
Lung	0.0062
Nerves	0.0029
Prostate	0.0192
Sensory organs	0.0000

2.1.3

Analogously to the procedure described under 2.1, the sequence Seq. ID No. 24 was found which occurs 5x more heavily in normal prostate tissue than in the tumor tissue.

The possible function of this gene area relates to the counterpart of an unknown gene yeast chromosome XVI.

The result is as follows:

Electronic Northern Blot for Seq. ID No.: 24

	NORMAL % freq.	TUMOR % freq.	Ratios N/T T/N	
Bladder	0.0000	0.0153	0.0000	undef
Breast	0.0120	0.0131	0.9174	1.0901
Ovary	0.0091	0.0208	0.4382	2.2819
Endocrine tissue	0.0145	0.0191	0.7655	1.3064
Gastrointestinal	0.0233	0.0143	1.6285	0.6141
Brain	0.0034	0.0077	0.4423	2.2607
Hematopoietic	0.0056	0.0000	undef	0.0000
Skin	0.0145	0.0847	0.1762	5.6754
Hepatic	0.0000	0.0518	0.0000	undef
Heart	0.0095	0.0275	0.3468	2.8832
Testicles	0.0061	0.0234	0.2612	3.8288
Lung	0.0100	0.0165	0.6020	1.6612
Stomach-esophagus	0.0097	0.0153	0.6300	1.5874
Muscle-skeleton	0.0051	0.0180	0.2855	3.5025
Kidney	0.0059	0.0000	undef	0.0000
Pancreas	0.0038	0.0221	0.1714	5.8337
Penis	0.0000	0.0267	0.0000	undef
Prostate	0.0214	0.0043	5.0338	0.1987
Uterus	0.0116	0.0142	0.8123	1.2211
Breast hyperplasia	0.0182			
Small intestine	0.0093			
Prostate hyperplasia	0.0178			
Seminal vesicle	0.0089			
Sensory organs	0.0000			
White blood cells	0.0061			

FETUS
% freq.

Development	0.0307
Gastrointestinal	0.0123
Brain	0.0125
Hematopoietic	0.0118
Heart-blood vessels	0.0082
Lung	0.0000
Kidney	0.0062
Prostate	0.0000
Sensory organs	0.0140

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0136
Ovary-uterus	0.0068
Endocrine tissue	0.0245
Fetal	0.0041
Gastrointestinal	0.0122
Hematopoietic	0.0057
Skin-muscle	0.0032
Testicles	0.0000
Lung	0.0000
Nerves	0.0010
Prostate	0.0000
Sensory organs	0.0000

2.1.4

Analogously to the procedure described under 2.1, the sequence Seq. ID No. 30 was found which occurs 4x more heavily in normal prostate tissue than in the tumor tissue.

The possible function of this gene area relates to the counterpart of a gene of thaliana of *Caenorhabditis elegans*.

The result is as follows:

Electronic Northern Blot for Seq. ID No.: 30

	NORMAL % freq.	TUMOR % freq.	Ratios N/T T/N	
Bladder	0.0000	0.0051	0.0000	undef
Breast	0.0040	0.0022	1.8347	0.5450
Ovary	0.0152	0.0026	5.8431	0.1711
Endocrine tissue	0.0000	0.0054	0.0000	undef
Gastrointestinal	0.0019	0.0000	undef	0.0000
Brain	0.0025	0.0044	0.5806	1.7224
Hematopoietic	0.0056	0.0000	undef	0.0000
Skin	0.0000	0.3000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0025	0.0024	1.0534	0.9493
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0034	0.0000	undef	0.0000
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0095	0.0021	4.4745	0.2235
Uterus	0.0017	0.0000	undef	0.0000
Breast hyperplasia	0.0000			
Small intestine	0.0031			
Prostate hyperplasia	0.0030			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0009			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0092
Brain	0.0000
Hematopoietic	0.0039
Heart-blood vessels	0.0000
Lung	0.0000
Kidney	0.0000
Prostate	0.0249
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0068
Ovary-uterus	0.0000
Endocrine tissue	0.0245
Fetal	0.0006
Gastrointestinal	0.0000
Hematopoietic	0.0057
Skin-muscle	0.0000
Testicles	0.0000
Lung	0.0000
Nerves	0.0000
Prostate	0.0030
Sensory organs	0.0192
	0.0000

2.1.5

Analogously to the procedure described under 2.1, the sequence Seq. ID No. 43 was found which occurs 6x more heavily in normal prostate tissue than in the tumor tissue.

The result is as follows:

Electronic Northern Blot for Seq. ID No.: 43

	NORMAL % freq.	TUMOR % freq.	Ratios N/T T/N	
Bladder	0.0000	0.0000	undef	undef
Breast	0.0120	0.0044	2.7521	0.3634
Ovary	0.0000	0.0026	0.0000	undef
Endocrine tissue	0.0018	0.0027	0.6698	1.4930
Gastrointestinal	0.0058	0.0048	1.2214	0.8187
Brain	0.0051	0.0000	undef	0.0000
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0032	0.0000	undef	0.0000
Testicles	0.0122	0.0000	undef	0.0000
Lung	0.0012	0.0024	0.5267	1.8996
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0060	0.0000	undef
Kidney	0.0059	0.0068	0.8683	1.1517
Pancreas	0.0000	0.0000	undef	undef
Prostate	0.0030	0.0000	undef	0.0000
Uterus	0.0119	0.0021	5.5932	0.1788
Breast hyperplasia	0.0050	0.0000	undef	0.0000
Small intestine	0.0145			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0030			
Sensory organs	0.0000			
White blood cells	0.0000			
	0.0035			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0031
Brain	0.0000
Hematopoietic	0.0039
Heart-blood vessels	0.0000
Lung	0.0037
Kidney	0.0062
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Ovary-uterus	0.0137
Endocrine tissue	0.0000
Fetal	0.0035
Gastrointestinal	0.0000
Hematopoietic	0.0057
Skin-muscle	0.0065
Testicles	0.0078
Lung	0.0000
Nerves	0.0050
Prostate	0.0000
Sensory organs	0.0000

2.1.5

Analogously to the procedure described under 2.1, the sequence Seq. ID No. 59 was found which occurs 5x more heavily in normal prostate tissue than in the tumor tissue.

The result is as follows:

Electronic Northern Blot for Seq. ID No.: 59

	NORMAL % freq.	TUMOR % freq.	Ratios N/T T/N	
Bladder	0.0093	0.0051	1.8185	0.5499
Breast	0.0067	0.0022	3.0579	0.3270
Ovary	0.0000	0.0052	0.0000	undef
Endocrine tissue	0.0091	0.0027	3.3489	0.2986
Gastrointestinal	0.0058	0.0000	undef	0.0000
Brain	0.0068	0.0088	0.7741	1.2918
Hematopoietic	0.0056	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0050	0.0000	undef	0.0000
Heart	0.0053	0.0000	undef	0.0000
Testicles	0.0183	0.0117	1.5671	0.6381
Lung	0.0062	0.0000	undef	0.0000
Stomach-esophagus	0.0057	0.0000	undef	0.0000
Muscle-skeleton	0.0154	0.0180	0.8565	1.1675
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0057	0.0166	0.3428	2.9168
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0333	0.0064	5.2203	0.1916
Uterus	0.0132	0.0000	undef	0.0000
Breast hyperplasia	0.0145			
Small intestine	0.0125			
Prostate hyperplasia	0.0149			
Seminal vesicle	0.0089			
Sensory organs	0.0000			
White blood cells	0.0131			

FETUS % freq.

Development	0.0000
Gastrointestinal	0.0123
Brain	0.0000
Hematopoietic	0.0000
Heart-blood vessels	0.0123
Lung	0.0148
Kidney	0.0062
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES % frequency

Breast	0.0272
Ovary-uterus	0.0068
Endocrine tissue	0.0245
Fetal	0.0082
Gastrointestinal	
Hematopoietic	0.0244
Skin-muscle	0.0000
Testicles	0.0259
Lung	0.0000
Nerves	0.0000
Prostate	0.0000
Sensory organs	0.0010
	0.0064
	0.0000

In an analogous procedure, the following Northern blots were also found:

Electronic Northern Blot for Seq. ID No.: 2			
	NORMAL	TUMOR	Ratios
	% freq.	% freq.	N/T T/N
Bladder	0.0418	0.0383	1.0911 0.9165
Breast	0.0267	0.0218	1.2232 0.8176
Ovary	0.0122	0.0052	2.3372 0.4279
Endocrine tissue	0.0055	0.0109	0.5023 1.9907
Gastrointestinal	0.0136	0.0048	2.8499 0.3509
Brain	0.0093	0.0142	0.6550 1.5267
Hematopoietic	0.0224	0.0000	undef 0.0000
Skin	0.0099	0.0847	0.1175 8.5131
Hepatic	0.0000	0.0129	0.0000 undef
Heart	0.0180	0.0000	undef 0.0000
Testicles	0.0061	0.0234	0.2612 3.8289
Lung	0.0137	0.0071	1.9313 0.5178
Stomach-esophagus	0.0193	0.0230	0.8399 1.1905
Muscle-skeleton	0.0103	0.0060	1.7130 0.5838
Kidney	0.0099	0.0000	undef 0.0000
Pancreas	0.0076	0.0110	0.6857 1.4584
Penis	0.0269	0.0000	undef 0.0000
Prostate	0.0143	0.0021	6.7118 0.1490
Uterus	0.0453	0.0356	1.2997 0.7694
Breast hyperplasia	0.0109		
Small intestine	0.0312		
Prostate hyperplasia	0.0238		
Seminal vesicle	0.0267		
Sensory organs	0.0353		
White blood cells	0.0174		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0123
Brain	0.0125
Hematopoietic	0.0039
Heart-blood vessels	0.0041
Lung	0.0370
Kidney	0.0124
Prostate	0.0748
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.1156
Ovary-uterus	0.0525
Endocrine tissue	0.0245
Fetal	0.0082
Gastrointestinal	0.0366
Hematopoietic	0.0000
Skin-muscle	0.0194
Testicles	0.0000
Lung	0.0082
Nerves	0.0151
Prostate	0.0385
Sensory organs	0.0000

Electronic Northern Blot for SEQ. ID. NO: 3

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
Bladder	0.0000	0.0000	undef	undef
Breast	0.0093	0.0022	4.2811	0.2336
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0109	0.0027	4.0187	0.2486
Gastrointestinal	0.0039	0.0000	undef	0.0000
Brain	0.0068	0.0077	0.8847	1.1303
Hematopoietic	0.0028	0.0000	undef	0.0000
Skin	0.0050	0.0000	undef	0.0000
Hepatic	0.0099	0.0065	1.5303	0.6535
Heart	0.0064	0.0000	undef	0.0000
Testicles	0.0061	0.0000	undef	0.0000
Lungs	0.0050	0.0000	undef	0.0000
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0051	0.0000	undef	0.0000
Kidneys	0.0030	0.0137	0.2171	4.6066
Pancreas	0.0019	0.0000	undef	0.0000
Penis	0.0120	0.0000	undef	0.0000
Prostate	0.0095	0.0043	2.2373	0.4470
Uterus	0.0017	0.0000	undef	0.0000
Breast hyperplasia	0.0036			
Small intestine	0.0000			
Prostatic hyperplasia	0.0059			
Seminal vesicles	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			

FETUS
% freq.

Development	0.0154
Gastrointestinal	0.0031
Brain	0.0000
Hematopoietic	0.0000
Heart-blood vessels	0.0082
Lungs	0.0000
Kidneys	0.0062
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0136
Ovary-uterus	0.0068
Endocrine tissue	0.0245
Fetal	0.0035
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0162
Testicles	0.0156
Lungs	0.0000
Nerves	0.0030
Prostate	0.0192
Sensory organs	0.0000

Electronic Northern Blot for SEQ. ID. NO: 4

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
Bladder	0.0093	0.0051	1.8185 0.5499
Breast	0.0053	0.0022	2.4463 0.4088
Gastrointestinal	0.0030	0.0026	1.1686 0.8557
Ovary	0.0055	0.0000	undef 0.0000
Endocrine tissue	0.0019	0.0000	undef 0.0000
Gastrointestinal	0.0008	0.0055	0.1548 6.4591
Brain	0.0000	0.0000	undef undef
Hematopoietic	0.0050	0.0000	undef undef
Skin	0.0000	0.0065	0.0000 undef
Hepatic	0.0053	0.0000	undef 0.0000
Heart	0.0000	0.0000	undef undef
Testicles	0.0050	0.0000	undef 0.0000
Lungs	0.0000	0.0000	undef undef
Stomach-esophagus	0.0051	0.0000	undef 0.0000
Muscle-skeleton	0.0089	0.0000	undef 0.0000
Kidneys	0.0038	0.0055	0.6857 1.4584
Pancreas	0.0000	0.0000	undef undef
Penis	0.0048	0.0021	2.2373 0.4470
Prostate	0.0116	0.0000	undef 0.0000
Uterus	0.0000		
Breast hyperplasia	0.0000		
Small intestine	0.0178		
Prostatic hyperplasia	0.0000		
Seminal vesicles	0.0000		
Sensory organs	0.0000		
White blood cells	0.0000		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0000
Heart-blood vessels	0.0000
Lungs	0.0062
Kidneys	0.0000
Prostate	0.0279
Sensory organs	

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Ovary-uterus	0.0137
Endocrine tissue	0.0000
Fetal	0.0134
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0518
Testicles	0.0000
Lungs	0.0000
Nerves	0.0050
Prostate	0.0128
Sensory organs	0.0000

Electronic Northern Blot for SEQ. ID. NO: 6

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
Bladder	0.0046	0.0026	1.8185 0.5499
Breast	0.0053	0.0022	2.4463 0.4088
Breast	0.0030	0.0026	1.1686 0.8557
Ovary	0.0055	0.0109	0.5023 1.9907
Endocrine tissue	0.0136	0.0048	2.8499 0.3509
Gastrointestinal	0.0068	0.0066	1.0321 0.9689
Brain	0.0098	0.0000	undef 0.0000
Hematopoietic	0.0000	0.0000	undef undef
Skin	0.0050	0.0129	0.3826 2.6139
Hepatic	0.0074	0.0000	undef 0.0000
Heart	0.0061	0.0117	0.5224 1.9144
Testicles	0.0100	0.0024	4.2137 0.2373
Lungs	0.0000	0.0000	undef undef
Stomach-esophagus	0.0051	0.0000	undef 0.0000
Muscle-skeleton	0.0059	0.0068	0.8683 1.1517
Kidneys	0.0170	0.0055	3.0855 0.3241
Pancreas	0.0030	0.0000	undef 0.0000
Penis	0.0095	0.0021	4.4745 0.2235
Prostate	0.0017	0.0142	0.1160 8.6176
Uterus	0.0036		
Breast hyperplasia	0.0062		
Small intestine	0.0000		
Prostatic hyperplasia	0.0000		
Seminal vesicles	0.0000		
Sensory organs	0.0000		
White blood cells	0.0096		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0125
Hematopoietic	0.0079
Heart-blood vessels	0.0123
Lungs	0.0037
Kidneys	0.0062
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0204
Ovary-uterus	0.0205
Endocrine tissue	0.0000
Fetal	0.0052
Gastrointestinal	0.0000
Hematopoietic	0.0057
Skin-muscle	0.0130
Testicles	0.0234
Lungs	0.0000
Nerves	0.0070
Prostate	0.0128
Sensory organs	0.0000

Electronic Northern Blot for SEQ. ID. NO: 7

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
Bladder	0.0093	0.0077	1.2123 0.8249
Breast	0.0107	0.0131	0.8154 1.2263
Breast	0.0030	0.0078	0.3895 2.5671
Ovary	0.0146	0.0000	undef 0.0000
Endocrine tissue	0.0097	0.0143	0.6786 1.4737
Gastrointestinal	0.0170	0.0088	1.9353 0.5167
Brain	0.0098	0.0378	0.2587 3.8650
Hematopoietic	0.0298	0.0000	undef 0.0000
Skin	0.0000	0.0194	0.0000 undef
Hepatic	0.0159	0.0137	1.1561 0.8650
Heart	0.0061	0.0000	undef 0.0000
Testicles	0.0112	0.0142	0.7901 1.2657
Lungs	0.0000	0.0153	0.0000 undef
Stomach-esophagus	0.0051	0.0060	0.8565 1.1675
Muscle-skeleton	0.0178	0.0068	2.6050 0.3839
Pancreas	0.0038	0.0387	0.0980 10.2089
Penis	0.0120	0.0000	undef 0.0000
Prostate	0.0095	0.0021	4.4745 0.2235
Uterus	0.0099	0.0000	undef 0.0000
Breast hyperplasia	0.0109		
Small intestine	0.0125		
Prostatic hyperplasia	0.0119		
Seminal vesicles	0.0356		
Sensory organs	0.0000		
White blood cells	0.0096		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0031
Brain	0.0188
Brain	0.0039
Hematopoietic	0.0000
Heart-blood vessels	0.0148
Lungs	0.0185
Kidneys	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0068
Ovary-uterus	0.0068
Ovary-uterus	0.0000
Endocrine tissue	0.0023
Fetal	0.0244
Gastrointestinal	0.0057
Hematopoietic	0.0162
Skin-muscle	0.0078
Testicles	0.0492
Lungs	0.0161
Nerves	0.0192
Prostate	0.0077
Sensory organs	

Electronic Northern Blot for SEQ. ID. NO: 8

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
Bladder	0.0000	0.0000	undef undef
Breast	0.0120	0.0109	1.1008 0.9084
Ovary	0.0061	0.0052	1.1686 0.8557
Endocrine tissue	0.0146	0.0136	1.0716 0.9331
Gastrointestinal	0.0155	0.0143	1.0857 0.9211
Brain	0.0136	0.0142	0.9527 1.0496
Hematopoietic	0.0042	0.0000	undef 0.0000
Skin	0.0050	0.0065	0.7651 1.3069
Hepatic	0.0170	0.0000	undef 0.0000
Heart	0.0000	0.0117	0.0000 undef
Testicles	0.0112	0.0095	1.1851 0.8438
Lungs	0.0000	0.0000	undef undef
Stomach-esophagus	0.0051	0.0060	0.8565 1.1675
Muscle-skeleton	0.0119	0.0068	1.7366 0.5758
Kidneys	0.0038	0.0000	undef 0.0000
Pancreas	0.0120	0.0000	undef 0.0000
Penis	0.0143	0.0064	2.2373 0.4470
Prostate	0.0033	0.0000	undef 0.0000
Uterus	0.0056		
Breast hyperplasia	0.0000		
Small intestine	0.0030		
Prostatic hyperplasia	0.0030		
Seminal vesicles	0.0089		
Sensory organs	0.0000		
White blood cells	0.0113		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0123
Brain	0.0063
Hematopoietic	0.0000
Heart-blood vessels	0.0164
Lungs	0.0037
Kidneys	0.0185
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0068
Ovary-uterus	0.0046
Endocrine tissue	0.0000
Fetal	0.0070
Gastrointestinal	0.0122
Hematopoietic	0.0114
Skin-muscle	0.0291
Testicles	0.0156
Lungs	0.0082
Nerves	0.0191
Prostate	0.0064
Sensory organs	0.0155

Electronic Northern Blot for SEQ. ID. NO: 9

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
Bladder	0.0232	0.0026	9.0924 0.1100
Breast	0.0187	0.0087	2.1405 0.4672
Breast	0.0122	0.0156	0.7791 1.2836
Ovary	0.0219	0.0136	1.6075 0.6221
Endocrine tissue	0.0116	0.0190	0.6107 1.6375
Gastrointestinal	0.0119	0.0142	0.8337 1.1995
Brain	0.0126	0.0000	undef 0.0000
Hematopoietic	0.0159	0.0000	undef 0.0000
Skin	0.0099	0.0000	undef 0.0000
Hepatic	0.0159	0.0137	1.1561 0.8650
Heart	0.0122	0.0351	0.3482 2.6716
Testicles	0.0187	0.0378	0.4938 2.0251
Lungs	0.0097	0.0307	0.3150 3.1749
Stomach-esophagus	0.0103	0.0120	0.8565 1.1675
Muscle-skeleton	0.0238	0.0000	undef 0.0000
Kidneys	0.0076	0.0055	1.3713 0.7292
Pancreas	0.0180	0.0267	0.6739 1.4840
Penis	0.0214	0.0085	2.5169 0.3973
Prostate	0.0132	0.0285	0.4642 2.1544
Uterus	0.0156		
Breast hyperplasia	0.0281		
Small intestine	0.0156		
Prostatic hyperplasia	0.0248		
Seminal vesicles	0.0356		
Sensory organs	0.0235		
White blood cells	0.0131		

FETUS
% freq.

Development	0.0307
Gastrointestinal	0.0247
Brain	0.0063
Brain	0.0236
Hematopoietic	0.0286
Heart-blood vessels	0.0111
Lungs	0.0371
Kidneys	0.0997
Prostate	0.0279
Sensory organs	

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0068
Ovary-uterus	0.0023
Endocrine tissue	0.0000
Fetal	0.0064
Gastrointestinal	0.0122
Hematopoietic	0.0057
Skin-muscle	0.0065
Testicles	0.0312
Lungs	0.0082
Nerves	0.0050
Prostate	0.0064
Sensory organs	0.0000

Electronic Northern Blot for SEQ. ID. NO: 12

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
Bladder	0.0000	0.0000	undef undef
Breast	0.0027	0.0044	0.6116 1.6351
Ovary	0.0000	0.0156	0.0000 undef
Endocrine tissue	0.0018	0.0027	0.6698 1.4930
Gastrointestinal	0.0078	0.0000	undef 0.0000
Brain	0.0034	0.0011	3.0964 0.3230
Hematopoietic	0.0000	0.0000	undef undef
Skin	0.0050	0.0000	undef 0.0000
Hepatic	0.0053	0.0000	undef 0.0000
Heart	0.0000	0.0000	undef undef
Testicles	0.0112	0.0000	undef 0.0000
Lungs	0.0000	0.0000	undef undef
Stomach-esophagus	0.0034	0.0060	0.5710 1.7513
Muscle-skeleton	0.0089	0.0068	1.3025 0.7678
Kidneys	0.0076	0.0000	undef 0.0000
Pancreas	0.0000	0.0000	undef undef
Penis	0.0048	0.0021	2.2373 0.4470
Prostate	0.0017	0.0000	undef 0.0000
Uterus	0.0036		
Breast hyperplasia	0.0156		
Small intestine	0.0089		
Prostatic hyperplasia	0.0000		
Seminal vesicles	0.0000		
Sensory organs	0.0000		
White blood cells	0.0052		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0031
Brain	0.0000
Hematopoietic	0.0000
Heart-blood vessels	0.0000
Lungs	0.0074
Kidneys	0.0000
Prostate	0.0000
Sensory organs	0.0140

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Ovary-uterus	0.0046
Endocrine tissue	0.0000
Fetal	0.0047
Gastrointestinal	0.0000
Hematopoietic	0.0057
Skin-muscle	0.0130
Testicles	0.0156
Lungs	0.0000
Nerves	0.0030
Prostate	0.0064
Sensory organs	0.0000

Electronic Northern Blot for SEQ. ID. NO: 13

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
Bladder	0.0000	0.0128	0.0000 undef
Breast	0.0120	0.0000	undef 0.0000
Breast	0.0000	0.0000	undef undef
Ovary	0.0036	0.0000	undef 0.0000
Endocrine tissue	0.0039	0.0000	undef 0.0000
Gastrointestinal	0.0017	0.0066	0.2580 3.8754
Brain	0.0000	0.0000	undef undef
Hematopoietic	0.0050	0.0000	undef 0.0000
Skin	0.0000	0.0129	0.0000 undef
Hepatic	0.0074	0.0000	undef 0.0000
Heart	0.0000	0.0117	0.0000 undef
Testicles	0.0087	0.0071	1.2290 0.8137
Lungs	0.0000	0.0000	undef undef
Stomach-esophagus	0.0086	0.0060	1.4275 0.7005
Muscle-skeleton	0.0000	0.0137	0.0000 undef
Kidneys	0.0038	0.0000	undef 0.0000
Pancreas	0.0150	0.0000	undef 0.0000
Penis	0.0048	0.0021	2.2373 0.4470
Prostate	0.0066	0.0071	0.9283 1.0772
Uterus	0.0218		
Breast hyperplasia	0.0062		
Small intestine	0.0030		
Prostatic hyperplasia	0.0089		
Seminal vesicles	0.0353		
Sensory organs	0.0000		
White blood cells			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0000
Heart-blood vessels	0.0041
Lungs	0.0000
Kidneys	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Ovary-uterus	0.0023
Endocrine tissue	0.0000
Fetal	0.0017
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0000
Lungs	0.0000
Nerves	0.0060
Prostate	0.0000
Sensory organs	0.0000

Electronic Northern Blot for SEQ. ID. NO: 14

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
Bladder	0.0046	0.0051	0.9082	1.0999
Breast	0.0027	0.0000	undef	0.0000
Ovary	0.0091	0.0000	undef	0.0000
Endocrine tissue	0.0018	0.0000	undef	0.0000
Gastrointestinal	0.0039	0.0000	undef	0.0000
Brain	0.0025	0.0022	1.1612	0.8612
Hematopoietic	0.0014	0.0000	undef	0.0000
Skin	0.0050	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0021	0.0137	0.1541	6.4872
Testicles	0.0000	0.0117	0.0000	undef
Lungs	0.0012	0.0024	0.5267	1.8986
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0051	0.0000	undef	0.0000
Kidneys	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0167	0.0000	undef	0.0000
Uterus	0.0017	0.0071	0.2321	4.3088
Breast hyperplasia	0.0000			
Small intestine	0.0000			
Prostatic hyperplasia	0.0030			
Seminal vesicles	0.0000			
Sensory organs	0.0000			
White blood cells	0.0052			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0000
Heart-blood vessels	0.0000
Lungs	0.0000
Kidneys	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Ovary-uterus	0.0000
Endocrine tissue	0.0000
Fetal	0.0012
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0000
Lungs	0.0078
Nerves	0.0000
Prostate	0.0020
Sensory organs	0.0192
	0.0000

Electronic Northern Blot for SEQ. ID. NO: 16

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
Bladder	0.0046	0.0000	undef	0.0000
Breast	0.0120	0.0022	5.5042	0.1817
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0019	0.0048	0.4071	2.4562
Brain	0.0085	0.0219	0.3871	2.5836
Hematopoietic	0.0014	0.0000	undef	0.0000
Skin	0.0050	0.0000	undef	0.0000
Hepatic	0.0000	0.0259	0.0000	undef
Heart	0.0032	0.0000	undef	0.0000
Testicles	0.0122	0.0000	undef	0.0000
Lungs	0.0037	0.0000	undef	0.0000
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0223	0.0000	undef	0.0000
Kidneys	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0150	0.0000	undef	0.0000
Prostate	0.0071	0.0000	undef	0.0000
Uterus	0.0182	0.0000	undef	0.0000
Breast hyperplasia	0.0036			
Small intestine	0.0000			
Prostatic hyperplasia	0.0089			
Seminal vesicles	0.0267			
Sensory organs	0.0000			
White blood cells	0.0000			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0062
Brain	0.0000
Hematopoietic	0.0041
Heart-blood vessels	0.0037
Lungs	0.0124
Kidneys	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0272
Ovary-uterus	0.0046
Endocrine tissue	0.0245
Fetal	0.0047
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0000
Lungs	0.0000
Nerves	0.0050
Prostate	0.0128
Sensory organs	0.0000

Electronic Northern Blot for SEQ. ID. NO: 17

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
Bladder	0.0093	0.0026	3.6370	0.2750
Breast	0.0053	0.0065	0.8154	1.2263
Ovary	0.0000	0.0104	0.0000	undef
Endocrine tissue	0.0091	0.0000	undef	0.0000
Gastrointestinal	0.0019	0.0048	0.4071	2.4562
Brain	0.0017	0.0022	0.7741	1.2918
Hematopoietic	0.0042	0.0378	0.1109	9.0183
Skin	0.0050	0.0000	undef	0.0000
Hepatic	0.0000	0.0065	0.0000	undef
Heart	0.0106	0.0000	undef	0.0000
Testicles	0.0061	0.0000	undef	0.0000
Lungs	0.0112	0.0071	1.5801	0.6329
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0086	0.0060	1.4275	0.7005
Kidneys	0.0059	0.0068	0.8683	1.1517
Pancreas	0.0057	0.0000	undef	0.0000
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0095	0.0043	2.2373	0.4470
Uterus	0.0050	0.0071	0.6963	1.4363
Breast hyperplasia	0.0000			
Small intestine	0.0031			
Prostatic hyperplasia	0.0089			
Seminal vesicles	0.0089			
Sensory organs	0.0118			
White blood cells	0.0044			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0063
Hematopoietic	0.0039
Heart-blood vessels	0.0000
Lungs	0.0000
Kidneys	0.0062
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Ovary-uterus	0.0000
Endocrine tissue	0.0000
Fetal	0.0000
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0032
Testicles	0.0000
Lungs	0.0000
Nerves	0.0164
Prostate	0.0010
Sensory organs	0.0128
	0.0387

Electronic Northern Blot for SEQ. ID. NO: 19

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
Bladder	0.0093	0.0128	0.7274	1.3748
Breast	0.0080	0.0065	1.2232	0.8176
Breast	0.0091	0.0000	undef	0.0000
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0039	0.0000	undef	0.0000
Gastrointestinal	0.0042	0.0044	0.9676	1.0335
Brain	0.0070	0.0000	undef	0.0000
Hematopoietic	0.0050	0.0000	undef	0.0000
Skin	0.0000	0.0065	0.0000	undef
Hepatic	0.0032	0.0137	0.2312	4.3248
Heart	0.0000	0.0000	undef	undef
Testicles	0.0037	0.0118	0.3160	3.1643
Lungs	0.0000	0.0153	0.0000	undef
Stomach-esophagus	0.0051	0.0000	undef	0.0000
Muscle-skeleton	0.0089	0.0000	undef	0.0000
Kidneys	0.0019	0.0055	0.3428	2.9168
Pancreas	0.0030	0.0000	undef	0.0000
Penis	0.0119	0.0064	1.8644	0.5364
Prostate	0.0099	0.0000	undef	0.0000
Uterus	0.0036			
Breast hyperplasia	0.0000			
Small intestine	0.0089			
Prostatic hyperplasia	0.0178			
Seminal vesicles	0.0000			
Sensory organs	0.0044			
White blood cells				

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0062
Brain	0.0000
Brain	0.0157
Hematopoietic	0.0082
Heart-blood vessels	0.0037
Lungs	0.0000
Kidneys	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0068
Ovary-uterus	0.0000
Endocrine tissue	0.0000
Petal	0.0047
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0000
Lungs	0.0000
Nerves	0.0000
Prostate	0.0192
Sensory organs	0.0155

Electronic Northern Blot for SEQ. ID. NO: 21

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
Bladder	0.0046	0.0128	0.3637	2.7495
Breast	0.0013	0.0087	0.1529	6.5404
Ovary	0.0061	0.0104	0.5843	1.7114
Endocrine tissue	0.0128	0.0136	0.9377	1.0664
Gastrointestinal	0.0078	0.0143	0.5428	1.8422
Brain	0.0102	0.0131	0.7741	1.2918
Hematopoietic	0.0042	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0129	0.0000	undef
Heart	0.0117	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lungs	0.0025	0.0165	0.1505	6.6450
Stomach-esophagus	0.0000	0.0230	0.0000	undef
Muscle-skeleton	0.0120	0.0120	0.9993	1.0007
Kidneys	0.0178	0.0068	2.6050	0.3839
Pancreas	0.0076	0.0210	0.6857	1.4584
Penis	0.0090	0.0267	0.3369	2.9680
Prostate	0.0167	0.0064	2.6101	0.3831
Uterus	0.0066	0.0214	0.3094	3.2316
Breast hyperplasia	0.0000			
Small intestine	0.0093			
Prostatic hyperplasia	0.0208			
Seminal vesicles	0.0267			
Sensory organs	0.0000			
White blood cells	0.0044			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0247
Brain	0.0188
Hematopoietic	0.0079
Heart-blood vessels	0.0245
Lungs	0.0037
Kidneys	0.0247
Prostate	0.0499
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0136
Ovary-uterus	0.0046
Endocrine tissue	0.0000
Fetal	0.0134
Gastrointestinal	0.0000
Hematopoietic	0.0114
Skin-muscle	0.0259
Testicles	0.0000
Lungs	0.0000
Nerves	0.0100
Prostate	0.0000
Sensory organs	0.0000

Electronic Northern Blot for SEQ. ID. NO: 23

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
Bladder	0.0093	0.0000	undef	0.0000
Breast	0.0013	0.0087	0.1529	6.5404
Ovary	0.0030	0.0078	0.3895	2.5671
Endocrine tissue	0.0036	0.0054	0.6698	1.4930
Gastrointestinal	0.0039	0.0048	0.8143	1.2281
Brain	0.0025	0.0033	0.7741	1.2518
Hematopoietic	0.0028	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0021	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lungs	0.0025	0.0047	0.5267	1.8986
Stomach-esophagus	0.0097	0.0000	undef	0.0000
Muscle-skeleton	0.0017	0.0060	0.2855	3.5025
Kidneys	0.0089	0.0068	1.3025	0.7678
Pancreas	0.0095	0.0055	1.7142	0.5834
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0024	0.0000	undef	0.0000
Uterus	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Small intestine	0.0000			
Prostatic hyperplasia	0.0149			
Seminal vesicles	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0031
Brain	0.0000
Hematopoietic	0.0000
Heart-blood vessels	0.0123
Lungs	0.0000
Kidneys	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Ovary-uterus	0.0000
Endocrine tissue	0.0000
Fetal	0.0000
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0000
Lungs	0.0082
Nerves	0.0010
Prostate	0.0192
Sensory organs	0.0000

Electronic Northern Blot for SEQ. ID. NO: 26

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
Bladder	0.0000	0.0026	0.0000	undef
Breast	0.0027	0.0044	0.6216	1.6351
Ovary	0.0061	0.0052	1.1696	0.8557
Endocrine tissue	0.0109	0.0027	4.0187	0.2488
Gastrointestinal	0.0019	0.0000	undef	0.0000
Brain	0.0068	0.0011	6.1926	0.1615
Hematopoietic	0.0028	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0129	0.0000	undef
Heart	0.0021	0.0000	undef	0.0000
Testicles	0.0122	0.0000	undef	0.0000
Lungs	0.0012	0.0071	0.1756	5.6957
Stomach-esophagus	0.0000	0.0077	0.0000	undef
Muscle-skeleton	0.0017	0.0060	0.2855	3.5025
Kidneys	0.0030	0.0068	0.4342	2.3033
Pancreas	0.0019	0.0000	undef	0.0000
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0119	0.0000	undef	0.0000
Uterus	0.0033	0.0000	undef	0.0000
Breast hyperplasia	0.0000			
Small intestine	0.0000			
Prostatic hyperplasia	0.0000			
Seminal vesicles	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
	0.0017			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0062
Brain	0.0000
Hematopoietic	0.0039
Heart-blood vessels	0.0000
Lungs	0.0000
Kidneys	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0068
Ovary-uterus	0.0183
Endocrine tissue	0.0000
Fetal	0.0122
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0032
Testicles	0.0078
Lungs	0.0000
Nerves	0.0030
Prostate	0.0064
Sensory organs	0.0000

Electronic Northern Blot for SEQ. ID. NO: 27

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
Bladder	0.0000	0.0000	undef	undef
Breast	0.0027	0.0022	1.2232	0.8176
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0018	0.0027	0.6698	1.4930
Gastrointestinal	0.0019	0.0000	undef	0.0000
Brain	0.0025	0.0022	1.1612	0.8612
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0011	0.0000	undef	0.0000
Testicles	0.0000	0.0117	0.0000	undef
Lungs	0.0025	0.0000	undef	0.0000
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidneys	0.0000	0.0000	undef	undef
Pancreas	0.0019	0.0000	undef	0.0000
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0071	0.0000	undef	0.0000
Uterus	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0036			
Small intestine	0.0000			
Prostatic hyperplasia	0.0000			
Seminal vesicles	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0063
Hematopoietic	0.0000
Heart-blood vessels	0.0037
Lungs	0.0062
Kidneys	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Ovary-uterus	0.0046
Endocrine tissue	0.0000
Fetal	0.0029
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0065
Testicles	0.0000
Lungs	0.0000
Nerves	0.0030
Prostate	0.0192
Sensory organs	0.0077

Electronic Northern Blot for SEQ. ID. NO: 28

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
Bladder	0.0000	0.0051	0.0000	undef
Breast	0.0040	0.0000	undef	0.000
Ovary	0.0030	0.0052	0.5843	1.7114
Endocrine tissue	0.0036	0.0027	1.3396	0.7465
Gastrointestinal	0.0058	0.0048	1.2214	0.8187
Brain	0.0017	0.0022	0.7741	1.2918
Hematopoietic	0.0028	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0129	0.0000	undef
Heart	0.0064	0.0000	undef	0.0000
Testicles	0.0183	0.0000	undef	0.0000
Lungs	0.0050	0.0024	2.1069	0.4746
Stomach-esophagus	0.0097	0.0077	1.2599	0.7937
Muscle-skeleton	0.0034	0.0000	undef	0.0000
Kidneys	0.0059	0.0000	undef	0.0000
Pancreas	0.0019	0.0110	0.1714	5.8337
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0119	0.0043	2.7966	0.3576
Uterus	0.0017	0.0000	undef	0.0000
Breast hyperplasia	0.0000			
Small intestine	0.0000			
Prostatic hyperplasia	0.0030			
Seminal vesicles	0.0000			
Sensory organs	0.0000			
White blood cells	0.0026			

FETUS
% freq.

Development	0.0154
Gastrointestinal	0.0031
Brain	0.0063
Hematopoietic	0.0000
Heart-blood vessels	0.0041
Lungs	0.0000
Kidneys	0.0000
Prostate	0.0249
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Ovary-uterus	0.0000
Endocrine tissue	0.0000
Fetal	0.0041
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0000
Lungs	0.0000
Nerves	0.0000
Prostate	0.0000
Sensory organs	0.0192
	0.0000

Electronic Northern Blot for SEQ. ID. NO: 29

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
Bladder	0.0000	0.0051	0.0000	undef
Breast	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0052	0.0000	undef
Endocrine tissue	0.0055	0.0000	undef	0.0000
Gastrointestinal	0.0019	0.0000	undef	0.0000
Brain	0.0093	0.0022	4.2576	0.2349
Hematopoietic	0.0028	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0050	0.0065	0.7651	1.3069
Heart	0.0042	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lungs	0.0025	0.0000	undef	0.0000
Stomach-esophagus	0.0000	0.0077	0.0000	undef
Muscle-skeleton	0.0017	0.0000	undef	0.0000
Kidneys	0.0059	0.0000	undef	0.0000
Pancreas	0.0000	0.0055	0.0000	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0048	0.0000	undef	0.0000
Uterus	0.0066	0.0000	undef	0.0000
Breast hyperplasia	0.0000			
Small intestine	0.0031			
Prostatic hyperplasia	0.0089			
Seminal vesicles	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			

FETUS
% freq.

Development	0.0154
Gastrointestinal	0.0031
Brain	0.0000
Hematopoietic	0.0000
Heart-blood vessels	0.0000
Lungs	0.0000
Kidneys	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Ovary-uterus	0.0137
Endocrine tissue	0.0000
Fetal	0.0017
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0078
Lungs	0.0000
Nerves	0.0000
Prostate	0.0141
Sensory organs	0.0256
	0.0077

Electronic Northern Blot for SEQ. ID. NO: 31

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0000	undef	undef
Ovary	0.0018	0.0000	undef	0.0000
Endocrine tissue	0.0019	0.0048	0.4071	2.4562
Gastrointestinal	0.0000	0.0022	0.0000	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lungs	0.0000	0.0024	0.0000	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0017	0.0000	undef	0.0000
Kidneys	0.0000	0.0000	undef	undef
Pancreas	0.0019	0.0000	undef	0.0000
Penis	0.0000	0.0000	undef	undef
Prostate	0.0095	0.0000	undef	0.0000
Uterus	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0073			
Small intestine	0.0000			
Prostatic hyperplasia	0.0000			
Seminal vesicles	0.0000			
Sensory organs	0.0000			
White blood cells	0.0009			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0000
Heart-blood vessels	0.0037
Lungs	0.0000
Kidneys	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Ovary-uterus	0.0000
Endocrine tissue	0.0000
Fetal	0.0029
Gastrointestinal	0.0122
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0000
Lungs	0.0000
Nerves	0.0000
Prostate	0.0064
Sensory organs	0.0000

Electronic Northern Blot for SEQ. ID. NO: 32

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
Bladder	0.0000	0.0026	0.0000	undef
Breast	0.0027	0.0022	1.2232	0.8176
Breast	0.0091	0.0078	1.1686	0.8557
Ovary	0.0055	0.0136	0.4019	2.4884
Endocrine tissue	0.0019	0.0095	0.2036	4.9124
Gastrointestinal	0.0076	0.0044	1.7417	0.5741
Brain	0.0028	0.0000	undef	0.0000
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0050	0.0000	undef	0.0000
Hepatic	0.0021	0.0000	undef	0.0000
Heart	0.0122	0.0000	undef	0.0000
Testicles	0.0012	0.0000	undef	0.0000
Lungs	0.0000	0.0000	undef	0.0000
Stomach-esophagus	0.0017	0.0180	0.0952	10.5076
Muscle-skeleton	0.0030	0.0068	0.4342	2.3033
Kidneys	0.0019	0.0000	undef	0.0000
Pancreas	0.0000	0.0000	undef	0.0000
Penis	0.0048	0.0000	undef	0.0000
Prostate	0.0017	0.0142	0.1160	8.6176
Uterus	0.0109			
Breast hyperplasia	0.0062			
Small intestine	0.0030			
Prostatic hyperplasia	0.0000			
Senial vesicles	0.0000			
Sensory organs	0.0000			
White blood cells	0.0017			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0154
Brain	0.0125
Brain	0.0000
Hematopoietic	0.0000
Heart-blood vessels	0.0000
Lungs	0.0000
Kidneys	0.0062
Prostate	0.0000
Sensory organs	0.0140

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Ovary-uterus	0.0045
Endocrine tissue	0.0000
Fetal	0.0128
Gastrointestinal	0.0000
Hematopoietic	0.0037
Skin-muscle	0.0097
Testicles	0.0468
Lungs	0.0082
Nerves	0.0060
Prostate	0.0192
Sensory organs	0.0232

Electronic Northern Blot for SEQ. ID. NO: 33

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
Bladder	0.0046	0.0026	1.8185 0.5499
Breast	0.0013	0.0022	0.6116 1.6351
Ovary	0.0000	0.0026	0.0000 undef
Endocrine tissue	0.0055	0.0000	undef 0.0000
Gastrointestinal	0.0019	0.0000	undef 0.0000
Brain	0.0042	0.0077	0.5529 1.8085
Hematopoietic	0.0000	0.0000	undef undef
Skin	0.0000	0.0000	undef undef
Hepatic	0.0000	0.0129	0.0000 undef
Heart	0.0000	0.0000	undef undef
Testicles	0.0000	0.0117	0.0000 undef
Lungs	0.0025	0.0047	0.5267 1.8986
Stomach-esophagus	0.0000	0.0000	undef undef
Muscle-skeleton	0.0000	0.0000	undef undef
Kidneys	0.0030	0.0000	undef 0.0000
Pancreas	0.0000	0.0000	undef undef
Penis	0.0030	0.0000	undef 0.0000
Prostate	0.0071	0.0021	3.3559 0.2980
Uterus	0.0017	0.0000	undef 0.0000
Breast hyperplasia	0.0000		
Small intestine	0.0062		
Prostatic hyperplasia	0.0119		
Seminal vesicles	0.0000		
Sensory organs	0.0000		
White blood cells	0.0017		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0063
Hematopoietic	0.0039
Heart-blood vessels	0.0041
Lungs	0.0000
Kidneys	0.0062
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Ovary-uterus	0.0023
Endocrine tissue	0.0000
Fetal	0.0017
Gastrointestinal	0.0244
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0000
Lungs	0.0000
Nerves	0.0030
Prostate	0.0000
Sensory organs	0.0000

Electronic Northern Blot for SEQ. ID. NO: 35

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
	0.0000	0.0026	0.0000 undef
Bladder	0.0093	0.0065	1.4270 0.7008
Breast	0.0091	0.0130	0.7012 1.4262
Ovary	0.0055	0.0027	2.0093 0.4977
Endocrine tissue	0.0039	0.0190	0.2036 4.9124
Gastrointestinal	0.0008	0.0033	0.2580 3.8754
Brain	0.0112	0.0000	undef 0.0000
Hematopoietic	0.0000	0.0000	undef undef
Skin	0.0000	0.0000	undef undef
Hepatic	0.0053	0.0137	0.3854 2.5949
Heart	0.0000	0.0000	undef undef
Testicles	0.0037	0.0024	1.5801 0.6329
Lungs	0.0000	0.0000	undef undef
Stomach-esophagus	0.0017	0.0060	0.2855 3.5025
Muscle-skeleton	0.0089	0.0137	0.6512 1.5355
Kidneys	0.0057	0.0000	undef 0.0000
Pancreas	0.0120	0.0000	undef 0.0000
Penis	0.0095	0.0021	4.4745 0.2235
Prostate	0.0033	0.0000	undef 0.0000
Uterus	0.0000		
Breast hyperplasia	0.0093		
Small intestine	0.0030		
Prostatic hyperplasia	0.0000		
Seminal vesicles	0.0118		
Sensory organs	0.0009		
White blood cells			

FETUS
% freq.

	0.0000
Development	0.0154
Gastrointestinal	0.0000
Brain	0.0039
Hematopoietic	0.0082
Heart-blood vessels	0.0074
Lungs	0.0000
Kidneys	0.0000
Prostate	0.0000
Sensory organs	

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

	0.0000
Breast	0.0297
Ovary-uterus	0.0245
Endocrine tissue	0.0082
Fetal	0.0000
Gastrointestinal	0.0057
Hematopoietic	0.0032
Skin-muscle	0.0156
Testicles	0.0000
Lungs	0.0080
Nerves	0.0064
Prostate	0.0000
Sensory organs	

Electronic Northern Blot for SEQ. ID. NO: 36

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
Bladder	0.0046	0.0077	0.6062 1.6497
Breast	0.0013	0.0153	0.0874 11.4458
Breast	0.0091	0.0026	3.5059 0.2852
Ovary	0.0036	0.0054	0.6698 1.4930
Endocrine tissue	0.0174	0.0048	3.6642 0.2729
Gastrointestinal	0.0034	0.0000	undef 0.0000
Brain	0.0028	0.0000	undef 0.0000
Hematopoietic	0.0249	0.0000	undef 0.0000
Skin	0.0248	0.0000	undef 0.0000
Hepatic	0.0032	0.0137	0.2312 4.3248
Heart	0.0000	0.0000	undef undef
Testicles	0.0261	0.0085	2.7652 0.3616
Lungs	0.0000	0.0000	undef undef
Stomach-esophagus	0.0000	0.0000	undef undef
Muscle-skeleton	0.0297	0.0000	undef 0.0000
Kidneys	0.0095	0.0000	undef 0.0000
Pancreas	0.0000	0.0000	undef undef
Penis	0.0143	0.0064	2.2373 0.4470
Prostate	0.0050	0.0000	undef 0.0000
Uterus	0.0145		
Breast hyperplasia	0.0031		
Small intestine	0.0149		
Prostatic hyperplasia	0.0089		
Seminal vesicles	0.0000		
Sensory organs	0.0000		
White blood cells	0.0000		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0031
Brain	0.0000
Brain	0.0039
Hematopoietic	0.0041
Heart-blood vessels	0.0074
Lungs	0.0000
Kidneys	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Ovary-uterus	0.0046
Endocrine tissue	0.0000
Fetal	0.0029
Gastrointestinal	0.0244
Hematopoietic	0.0000
Skin-muscle	0.0032
Testicles	0.0000
Lungs	0.0246
Nerves	0.0010
Prostate	0.0064
Sensory organs	0.0000

Electronic Northern Blot for SEQ. ID. NO: 37

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
Bladder	0.0093	0.0000	undef	0.0000
Breast	0.0013	0.0000	undef	0.000
Breast	0.0000	0.0000	undef	undef
Ovary	0.0018	0.0000	undef	0.0000
Endocrine tissue	0.0039	0.0000	undef	0.0000
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0011	0.0000	undef	0.0000
Heart	0.0000	0.0000	undef	undef
Testicles	0.0012	0.0000	undef	0.0000
Lungs	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidneys	0.0000	0.0000	undef	undef
Pancreas	0.0030	0.0000	undef	0.0000
Penis	0.0095	0.0021	4.4745	0.2235
Prostate	0.0050	0.0356	0.1393	7.1813
Uterus	0.0000			
Breast hyperplasia	0.0093			
Small intestine	0.0000			
Prostatic hyperplasia	0.0059			
Seminal vesicles	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			

	FETUS % freq.
Development	0.0000
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0000
Heart-blood vessels	0.0000
Lungs	0.0062
Kidneys	0.0000
Prostate	0.0000
Sensory organs	0.0000

	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Breast	0.0000
Ovary-uterus	0.0000
Endocrine tissue	0.0000
Fetal	0.0000
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0000
Lungs	0.0000
Nerves	0.0000
Prostate	0.0064
Sensory organs	0.0000

Electronic Northern Blot for SEQ. ID. NO: 39

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
Bladder	0.0325	0.0332	0.9792 1.0213
Breast	0.0293	0.0196	1.4950 0.6689
Ovary	0.0000	0.0104	0.0000 undef
Endocrine tissue	0.0091	0.0000	undef 0.0000
Gastrointestinal	0.0252	0.0000	undef 0.0000
Brain	0.0085	0.0131	0.6451 1.5502
Hematopoietic	0.0098	0.0000	undef 0.0000
Skin	0.0249	0.0000	undef 0.0000
Hepatic	0.0000	0.0065	0.0000 undef
Heart	0.0636	0.1649	0.3854 2.5949
Testicles	0.0183	0.0000	undef 0.0000
Lungs	0.0212	0.0165	1.2792 0.7818
Stomach-esophagus	0.0000	0.0153	0.0000 undef
Muscle-skeleton	0.0137	0.0060	2.2841 0.4378
Kidneys	0.0208	0.0137	1.5196 0.6581
Pancreas	0.0284	0.0166	1.7142 0.5834
Penis	0.0000	0.0533	0.0000 undef
Prostate	0.0048	0.0106	0.4475 2.2349
Uterus	0.0033	0.0000	undef 0.0000
Breast hyperplasia	0.0036		
Small intestine	0.0218		
Prostatic hyperplasia	0.0119		
Seminal vesicles	0.0000		
Sensory organs	0.0588		
White blood cells	0.1045		

FETUS
% freq.

Development	0.0154
Gastrointestinal	0.0123
Brain	0.0000
Hematopoietic	0.0118
Heart-blood vessels	0.0041
Lungs	0.0148
Kidneys	0.0000
Prostate	0.0249
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Ovary-uterus	0.0114
Endocrine tissue	0.1224
Fetal	0.0122
Gastrointestinal	0.0366
Hematopoietic	0.0000
Skin-muscle	0.0291
Testicles	0.0000
Lungs	0.0164
Nerves	0.0040
Prostate	0.0385
Sensory organs	0.0000

Electronic Northern Blot for SEQ. ID. NO: 41

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0022	0.0000	undef
Ovary	0.0061	0.0026	2.3372	0.4279
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	0.0000
Skin	0.0050	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lungs	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidneys	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0048	0.0000	undef	0.0000
Uterus	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Small intestine	0.0000			
Prostatic hyperplasia	0.0059			
Seminal vesicles	0.0000			
Sensory organs	0.0000			
White blood cells	0.0009			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0000
Heart-blood vessels	0.0037
Lungs	0.0000
Kidneys	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Ovary-uterus	0.0023
Endocrine tissue	0.0000
Fetal	0.0017
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0078
Lungs	0.0082
Nerves	0.0010
Prostate	0.0192
Sensory organs	0.0000

Electronic Northern Blot for SEQ. ID. NO: 42

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
	0.0000	0.0000	undef	undef
Bladder	0.0160	0.0044	3.6695	0.2725
Breast	0.0030	0.0026	1.1686	0.8557
Ovary	0.0109	0.0082	1.3396	0.7465
Endocrine tissue	0.0078	0.0000	undef	0.0000
Gastrointestinal	0.0042	0.0055	0.7741	1.2918
Brain	0.0070	0.0000	undef	0.0000
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0042	0.0000	undef	0.0000
Heart	0.0000	0.0000	undef	undef
Testicles	0.0037	0.0024	1.5801	0.6329
Lungs	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0060	0.0000	undef
Muscle-skeleton	0.0059	0.0000	undef	0.0000
Kidneys	0.0057	0.0000	undef	0.0000
Pancreas	0.0090	0.0000	undef	0.0000
Penis	0.0167	0.0000	undef	0.0000
Prostate	0.0066	0.0000	undef	0.0000
Uterus	0.0109	0.0000	undef	0.0000
Breast hyperplasia	0.0031			
Small intestine	0.0000			
Prostatic hyperplasia	0.0000			
Seminal vesicles	0.0000			
Sensory organs	0.0017			
White blood cells				

	FETUS % freq.
	0.0000
Development	0.0062
Gastrointestinal	0.0000
Brain	0.0039
Hematopoietic	0.0041
Heart-blood vessels	0.0000
Lungs	0.0000
Kidneys	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0136
Ovary-uterus	0.0023
Endocrine tissue	0.0000
Fetal	0.0070
Gastrointestinal	0.0000
Hematopoietic	0.0032
Skin-muscle	0.0000
Testicles	0.0000
Lungs	0.0000
Nerves	0.0020
Prostate	0.0256
Sensory organs	0.0000

Electronic Northern Blot for SEQ. ID. NO: 44

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
Bladder	0.0372	0.0230	1.6164 0.6186
Breast	0.0067	0.0000	undef 0.0000
Ovary	0.0122	0.0130	0.9349 1.0696
Endocrine tissue	0.0128	0.0300	0.4262 2.3462
Gastrointestinal	0.0271	0.0333	0.8143 1.2281
Brain	0.0059	0.0471	0.1260 7.9354
Hematopoietic	0.0058	0.0000	undef 0.0000
Skin	0.0099	0.0000	undef 0.0000
Hepatic	0.0050	0.0259	0.1913 5.2277
Heart	0.0201	0.0137	1.4644 0.6829
Testicles	0.0000	0.0117	0.0000 undef
Lungs	0.0274	0.0189	1.4485 0.6904
Stomach-esophagus	0.0290	0.0000	undef 0.0000
Muscle-skeleton	0.0103	0.0000	undef 0.0000
Kidneys	0.0089	0.0137	0.6512 1.5355
Pancreas	0.0076	0.0166	0.4571 2.1876
Penis	0.0150	0.0000	undef 0.0000
Prostate	0.0333	0.0106	3.1322 0.3193
Uterus	0.0215	0.0000	undef 0.0000
Breast hyperplasia	0.0036		
Small intestine	0.0280		
Prostatic hyperplasia	0.0357		
Seminal vesicles	0.0890		
Sensory organs	0.0235		
White blood cells	0.0052		

	FETUS % freq.
Development	0.0000
Gastrointestinal	0.0031
Brain	0.0000
Hematopoietic	0.0039
Heart-blood vessels	0.0041
Lungs	0.0222
Kidneys	0.0309
Prostate	0.0249
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Ovary-uterus	0.0183
Endocrine tissue	0.0000
Fetal	0.0227
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0162
Testicles	0.0000
Lungs	0.0082
Nerves	0.0050
Prostate	0.0256
Sensory organs	0.0000

Electronic Northern Blot for SEQ. ID. NO: 46

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
Bladder	0.0000	0.0026	0.0000 undef
Breast	0.0040	0.0131	0.3058 3.2702
Breast	0.0122	0.0234	0.5194 1.9254
Ovary	0.0036	0.0109	0.3349 2.9861
Endocrine tissue	0.0116	0.0095	1.2214 0.8187
Gastrointestinal	0.0051	0.0164	0.3096 3.2295
Brain	0.0028	0.0000	undef 0.0000
Hematopoietic	0.0050	0.0000	undef 0.0000
Skin	0.0050	0.0000	undef 0.0000
Hepatic	0.0085	0.0137	0.6166 1.6218
Heart	0.0061	0.0117	0.5224 1.9144
Testicles	0.0075	0.0095	0.7901 1.2657
Lungs	0.0000	0.0000	undef undef
Stomach-esophagus	0.0051	0.0000	undef 0.0000
Muscle-skeleton	0.0030	0.0068	0.4342 2.3033
Kidneys	0.0076	0.0055	1.3713 0.7292
Pancreas	0.0030	0.0000	undef 0.0000
Penis	0.0119	0.0043	2.7966 0.3576
Prostate	0.0083	0.0071	1.1604 0.8618
Uterus	0.0036		
Breast hyperplasia	0.0093		
Small intestine	0.0030		
Prostatic hyperplasia	0.0000		
Seminal vesicles	0.0118		
Sensory organs	0.0026		
White blood cells			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0154
Brain	0.0125
Hematopoietic	0.0157
Heart-blood vessels	0.0041
Lungs	0.0037
Kidneys	0.0062
Prostate	0.0000
Sensory organs	0.0140

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Ovary-uterus	0.0046
Endocrine tissue	0.0245
Fetal	0.0117
Gastrointestinal	0.0122
Hematopoietic	0.0000
Skin-muscle	0.0130
Testicles	0.0000
Lungs	0.0164
Nerves	0.0110
Prostate	0.0192
Sensory organs	0.0000

Electronic Northern Blot for SEQ. ID. NO: 47

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
Bladder	0.0093	0.0077	1.2123 0.8249
Breast	0.0093	0.0283	0.3293 3.0366
Ovary	0.0182	0.0052	3.5059 0.2852
Endocrine tissue	0.0000	0.0000	undef undef
Gastrointestinal	0.0504	0.0000	undef 0.0000
Brain	0.0000	0.0033	0.0000 undef
Hematopoietic	0.0042	0.0000	undef 0.0000
Skin	0.0050	0.0000	undef 0.0000
Hepatic	0.0495	0.0065	7.6515 0.1307
Heart	0.0074	0.0137	0.5395 1.8535
Testicles	0.0000	0.0000	undef undef
Lungs	0.0000	0.0000	undef undef
Stomach-esophagus	0.0000	0.0000	undef undef
Muscle-skeleton	0.0120	0.0060	1.9985 0.5004
Kidneys	0.0236	0.0000	undef 0.0000
Pancreas	0.0511	0.0276	1.8513 0.5402
Penis	0.0000	0.0000	undef undef
Prostate	0.0333	0.0149	2.2373 0.4470
Uterus	0.0017	0.0000	undef 0.0000
Breast hyperplasia	0.0109		
Small intestine	0.1028		
Prostatic hyperplasia	0.0059		
Seminal vesicles	0.0000		
Sensory organs	0.0000		
White blood cells	0.0000		
	0.0183		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0462
Brain	0.0000
Hematopoietic	0.0197
Heart-blood vessels	0.0000
Lungs	0.0000
Kidneys	0.0062
Prostate	0.0249
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Ovary-uterus	0.0160
Endocrine tissue	0.0000
Fetal	0.0122
Gastrointestinal	0.0122
Hematopoietic	0.0000
Skin-muscle	0.0324
Testicles	0.0000
Lungs	0.0000
Nerves	0.0000
Prostate	0.0256
Sensory organs	0.0000

Electronic Northern Blot for SEQ. ID. NO: 51

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
Bladder	0.0465	0.0741	0.6271 1.5947
Breast	0.0386	0.0501	0.7711 1.2968
Ovary	0.0334	0.0546	0.6121 1.6336
Endocrine tissue	0.0310	0.0300	1.0351 0.9661
Gastrointestinal	0.0252	0.0190	1.3232 0.7558
Brain	0.0458	0.0701	0.6532 1.5310
Hematopoietic	0.0112	0.1135	0.0986 10.1456
Skin	0.0448	0.0000	undef 0.0000
Hepatic	0.0347	0.0000	undef 0.0000
Heart	0.1123	0.1375	0.8170 1.2240
Testicles	0.0366	0.0468	0.7835 1.2763
Lungs	0.0535	0.0449	1.1920 0.8389
Stomach-esophagus	0.0193	0.0153	1.2599 0.7937
Muscle-skeleton	0.0685	0.1860	0.3684 2.7145
Kidneys	0.0119	0.0890	0.1336 7.4857
Pancreas	0.0151	0.0828	0.1828 5.4691
Penis	0.1018	0.0533	1.9092 0.5238
Prostate	0.0167	0.0064	2.6101 0.3831
Uterus	0.0545	0.2634	0.2070 4.8311
Breast hyperplasia	0.0981		
Small intestine	0.0312		
Prostatic hyperplasia	0.0386		
Seminal vesicles	0.0178		
Sensory organs	0.0235		
White blood cells	0.0009		

FETUS
% freq.

Development	0.1383
Gastrointestinal	0.0924
Brain	0.0063
Hematopoietic	0.0393
Heart-blood vessels	0.0654
Lungs	0.0592
Kidneys	0.0309
Prostate	0.2992
Sensory organs	0.0279

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0204
Ovary-uterus	0.0068
Endocrine tissue	0.0000
Fetal	0.0099
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0000
Lungs	0.0000
Nerves	0.0171
Prostate	0.0000
Sensory organs	0.0387

Electronic Northern Blot for SEQ. ID. NO: 52

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
Bladder	0.0000	0.0000	undef	undef
Breast	0.0013	0.0022	0.6116	1.6351
Ovary	0.0030	0.0000	undef	0.0000
Endocrine tissue	0.0036	0.0000	undef	0.0000
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0008	0.0099	0.0860	11.6263
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0032	0.0000	undef	0.0000
Testicles	0.0061	0.0000	undef	0.0000
Lungs	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidneys	0.0059	0.0000	undef	0.0000
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0119	0.0021	5.5932	0.1788
Uterus	0.0083	0.0000	undef	0.0000
Breast hyperplasia	0.0036			
Small intestine	0.0000			
Prostatic hyperplasia	0.0030			
Seminal vesicles	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0031
Brain	0.0000
Hematopoietic	0.0000
Heart-blood vessels	0.0037
Lungs	0.0000
Kidneys	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0136
Ovary-uterus	0.0114
Endocrine tissue	0.0000
Fetal	0.0017
Gastrointestinal	0.0122
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0000
Lungs	0.0000
Nerves	0.0040
Prostate	0.0000
Sensory organs	0.0000

Electronic Northern Blot for SEQ. ID. NO: 53

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
Bladder	0.0000	0.0051	0.0000 undef
Breast	0.0000	0.0044	0.0000 undef
Ovary	0.0030	0.0000	undef 0.0000
Endocrine tissue	0.0055	0.0027	2.0093 0.4977
Gastrointestinal	0.0058	0.0048	1.2214 0.8187
Brain	0.0000	0.0000	undef undef
Hematopoietic	0.0000	0.0000	undef undef
Skin	0.0000	0.0000	undef undef
Hepatic	0.0000	0.0000	undef undef
Heart	0.0032	0.0000	undef 0.0000
Testicles	0.0000	0.0000	undef undef
Lungs	0.0000	0.0024	0.0000 undef
Stomach-esophagus	0.0000	0.0153	0.0000 undef
Muscle-skeleton	0.0034	0.0000	undef undef
Kidneys	0.0000	0.0000	undef undef
Pancreas	0.0000	0.0000	undef undef
Penis	0.0000	0.0000	undef undef
Prostate	0.0071	0.0021	3.3559 0.2980
Uterus	0.0033	0.0000	undef 0.0000
Breast hyperplasia	0.0036		
Small intestine	0.0000		
Prostatic hyperplasia	0.0030		
Seminal vesicles	0.0000		
Sensory organs	0.0000		
White blood cells	0.0000		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0000
Heart-blood vessels	0.0037
Lungs	0.0062
Kidneys	0.0000
Prostate	0.0140
Sensory organs	

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Ovary-uterus	0.0046
Endocrine tissue	0.0000
Fetal	0.0000
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0032
Testicles	0.0000
Lungs	0.0000
Nerves	0.0030
Prostate	0.0128
Sensory organs	0.0000

Electronic Northern Blot for SEQ. ID. NO: 54

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
Bladder	0.0093	0.0077	1.2123 0.8249
Breast	0.0200	0.0044	4.5868 0.2180
Breast	0.0152	0.0104	1.4608 0.6846
Ovary	0.0091	0.0054	1.6745 0.5972
Endocrine tissue	0.0039	0.0048	0.8143 1.2281
Gastrointestinal	0.0110	0.0033	3.3545 0.2981
Brain	0.0056	0.0000	undef 0.0000
Hematopoietic	0.0149	0.0000	undef 0.0000
Skin	0.0198	0.0000	undef 0.0000
Hepatic	0.0064	0.0000	undef 0.0000
Heart	0.0122	0.0000	undef 0.0000
Testicles	0.0062	0.0071	0.8779 1.1391
Lungs	0.0097	0.0000	undef 0.0000
Stomach-esophagus	0.0051	0.0240	0.2141 4.6701
Muscle-skeleton	0.0178	0.0000	undef 0.0000
Kidneys	0.0019	0.0110	0.1714 5.8337
Pancreas	0.0060	0.0000	undef 0.0000
Penis	0.0119	0.0043	2.7966 0.3576
Prostate	0.0050	0.0214	0.2321 4.3088
Uterus	0.0000		
Breast hyperplasia	0.0062		
Small intestine	0.0208		
Prostatic hyperplasia	0.0000		
Seminal vesicles	0.0000		
Sensory organs	0.0000		
White blood cells	0.0540		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0123
Brain	0.0250
Brain	0.0275
Hematopoietic	0.0082
Heart-blood vessels	0.0037
Lungs	0.0185
Kidneys	0.0000
Prostate	0.0558
Sensory organs	

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0136
Ovary-uterus	0.0046
Endocrine tissue	0.0000
Fetal	0.0023
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0130
Testicles	0.0000
Lungs	0.0082
Nerves	0.0040
Prostate	0.0064
Sensory organs	0.0310

Electronic Northern Blot for SEQ. ID. NO: 55

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
Bladder	0.0093	0.0153	0.6062 1.6457
Breast	0.0053	0.0065	0.8154 1.2263
Breast	0.0000	0.0052	0.0000 undef
Ovary	0.0055	0.0054	1.0047 0.9954
Endocrine tissue	0.0039	0.0048	0.8143 1.2281
Gastrointestinal	0.0042	0.0033	1.2902 0.7751
Brain	0.0028	0.0000	undef 0.0000
Hematopoietic	0.0000	0.0000	undef undef
Skin	0.0050	0.0129	0.3826 2.6139
Hepatic	0.0074	0.0000	undef 0.0000
Heart	0.0061	0.0234	0.2612 3.8288
Testicles	0.0100	0.0095	1.0534 0.9493
Lungs	0.0000	0.0000	undef undef
Stomach-esophagus	0.0034	0.0000	undef 0.0000
Muscle-skeleton	0.0089	0.0137	0.6512 1.5355
Kidneys	0.0057	0.0000	undef 0.0000
Pancreas	0.0030	0.0000	undef 0.0000
Penis	0.0048	0.0021	2.2373 0.4470
Prostate	0.0066	0.0071	0.9283 1.0772
Uterus	0.0036		
Breast hyperplasia	0.0000		
Small intestine	0.0059		
Prostatic hyperplasia	0.0089		
Seminal vesicles	0.0118		
Sensory organs	0.0026		
White blood cells			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0031
Brain	0.0000
Hematopoietic	0.0000
Heart-blood vessels	0.0000
Lungs	0.0000
Kidneys	0.0062
Prostate	0.0249
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Ovary-uterus	0.0046
Endocrine tissue	0.0000
Fetal	0.0017
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0000
Lungs	0.0082
Nerves	0.0010
Prostate	0.0128
Sensory organs	0.0000

Electronic Northern Blot for SEQ. ID. NO: 58

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
Bladder	0.0093	0.0026	3.6370	0.2750
Breast	0.0080	0.0022	3.6695	0.2725
Ovary	0.0061	0.0078	0.7791	1.2836
Endocrine tissue	0.0018	0.0109	0.1674	5.9721
Gastrointestinal	0.0078	0.0143	0.5428	1.8422
Brain	0.0034	0.0033	1.0321	0.9689
Hematopoietic	0.0084	0.0000	undef	0.0000
Skin	0.0895	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0032	0.0137	0.2312	4.3248
Testicles	0.0183	0.0000	undef	0.0000
Lungs	0.0037	0.0142	0.2634	3.7971
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0051	0.0000	undef	0.0000
Kidneys	0.0000	0.0068	0.0000	undef
Pancreas	0.0038	0.0000	undef	0.0000
Penis	0.0090	0.0000	undef	0.0000
Prostate	0.0071	0.0021	3.3559	0.2980
Uterus	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0182			
Small intestine	0.0031			
Prostatic hyperplasia	0.0030			
Seminal vesicles	0.0000			
Sensory organs	0.0000			
White blood cells	0.0026			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0031
Brain	0.0000
Hematopoietic	0.0157
Heart-blood vessels	0.0082
Lungs	0.0148
Kidneys	0.0124
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Ovary-uterus	0.0160
Endocrine tissue	0.0245
Petal	0.0082
Gastrointestinal	0.0122
Hematopoietic	0.0057
Skin-muscle	0.0032
Testicles	0.0156
Lungs	0.0082
Nerves	0.0080
Prostate	0.0128
Sensory organs	0.0000

Electronic Northern Blot for SEQ. ID. NO: 60

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
Bladder	0.0046	0.0000	undef	0.0000
Breast	0.0040	0.0022	1.8347	0.5450
Ovary	0.0000	0.0026	0.0000	undef
Endocrine tissue	0.0000	0.0054	0.0000	undef
Gastrointestinal	0.0019	0.0000	undef	0.0000
Brain	0.0068	0.0033	2.0643	0.4844
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0050	0.0000	undef	0.0000
Heart	0.0011	0.0000	undef	0.0000
Testicles	0.0061	0.0000	undef	0.0000
Lungs	0.0050	0.0000	undef	0.0000
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidneys	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0060	0.0000	undef	0.0000
Prostate	0.0071	0.0000	undef	0.0000
Uterus	0.0017	0.0000	undef	0.0000
Breast hyperplasia	0.0073			
Small intestine	0.0000			
Prostatic hyperplasia	0.0059			
Seminal vesicles	0.0000			
Sensory organs	0.0235			
White blood cells	0.0026			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0039
Heart-blood vessels	0.0000
Lungs	0.0037
Kidneys	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Ovary-uterus	0.0046
Endocrine tissue	0.0000
Fetal	0.0000
Gastrointestinal	0.0122
Hematopoietic	0.0000
Skin-muscle	0.0032
Testicles	0.0000
Lungs	0.0000
Nerves	0.0010
Prostate	0.0000
Sensory organs	0.0000

Electronic Northern Blot for SEQ. ID. NO: 61

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
Bladder	0.0000	0.0128	0.0000 undef
Breast	0.0000	0.0022	0.0000 undef
Ovary	0.0000	0.0000	undef undef
Endocrine tissue	0.0018	0.0109	0.1674 5.9721
Gastrointestinal	0.0078	0.0000	undef 0.0000
Brain	0.0034	0.0033	1.0321 0.9689
Hematopoietic	0.0000	0.0000	undef undef
Skin	0.0000	0.0000	undef undef
Hepatic	0.0050	0.0000	undef 0.0000
Heart	0.0032	0.0000	undef 0.0000
Testicles	0.0183	0.0000	undef 0.0000
Lungs	0.0025	0.0071	0.3511 2.8478
Stomach-esophagus	0.0000	0.0000	undef undef
Muscle-skeleton	0.0051	0.0000	undef 0.0000
Kidneys	0.0000	0.0000	undef undef
Pancreas	0.0019	0.0110	0.1714 5.8337
Penis	0.0120	0.0000	undef 0.0000
Prostate	0.0071	0.0021	3.3559 0.2980
Uterus	0.0033	0.0000	undef 0.0000
Breast hyperplasia	0.0000		
Small intestine	0.0093		
Prostatic hyperplasia	0.0030		
Seminal vesicles	0.0000		
Sensory organs	0.0000		
White blood cells	0.0009		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0188
Hematopoietic	0.0000
Heart-blood vessels	0.0041
Lungs	0.0037
Kidneys	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0136
Ovary-uterus	0.0046
Endocrine tissue	0.0000
Fetal	0.0000
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0000
Lungs	0.0154
Nerves	0.0050
Prostate	0.0192
Sensory organs	0.0000

Electronic Northern Blot for SEQ. ID. NO: 62

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
Bladder	0.0046	0.0026	1.8185 0.5499
Breast	0.0133	0.0022	6.1158 0.1635
Ovary	0.0061	0.0052	1.1686 0.8557
Endocrine tissue	0.0000	0.0245	0.0000 undef
Gastrointestinal	0.0078	0.0190	0.4071 2.4562
Brain	0.0119	0.0022	5.4187 0.1845
Hematopoietic	0.0070	0.0757	0.0924 10.8219
Skin	0.0050	0.0000	undef 0.0000
Hepatic	0.0099	0.0000	undef 0.0000
Heart	0.0074	0.0275	0.2698 3.7070
Testicles	0.0000	0.0234	0.0000 undef
Lungs	0.0050	0.0118	0.4214 2.3732
Stomach-esophagus	0.0097	0.0153	0.6300 1.5874
Muscle-skeleton	0.0034	0.0000	undef 0.0000
Kidneys	0.0119	0.0205	0.5789 1.7275
Pancreas	0.0038	0.0000	undef 0.0000
Penis	0.0060	0.0000	undef 0.0000
Prostate	0.0191	0.0043	4.4745 0.2235
Uterus	0.0066	0.0000	undef 0.0000
Breast hyperplasia	0.0000		
Small intestine	0.0031		
Prostatic hyperplasia	0.0059		
Seminal vesicles	0.0000		
Sensory organs	0.0000		
White blood cells	0.0070		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0031
Brain	0.0000
Hematopoietic	0.0082
Heart-blood vessels	0.0037
Lungs	0.0309
Kidneys	0.0000
Prostate	0.0140
Sensory organs	

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0068
Ovary-uterus	0.0183
Endocrine tissue	0.0000
Fetal	0.0140
Gastrointestinal	0.0244
Hematopoietic	0.0000
Skin-muscle	0.0194
Testicles	0.0000
Lungs	0.0000
Nerves	0.0161
Prostate	0.0128
Sensory organs	0.0155

Electronic Northern Blot for SEQ. ID. NO: 63

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
Bladder	0.0186	0.0844	0.2204 4.5368
Breast	0.0560	0.0370	1.5110 0.6618
Breast	0.0395	0.0260	1.5192 0.6582
Ovary	0.0128	0.0245	0.5209 1.9196
Endocrine tissue	0.0775	0.0857	0.9047 1.1053
Gastrointestinal	0.0254	0.0350	0.7257 1.3779
Brain	0.0364	0.0378	0.9610 1.0406
Hematopoietic	0.2188	0.0000	undef 0.0000
Skin	0.0198	0.0582	0.3401 2.9406
Hepatic	0.1112	0.1787	0.6225 1.6064
Heart	0.0183	0.0117	1.5671 0.6381
Testicles	0.1133	0.0804	1.4097 0.7094
Lungs	0.0676	0.0307	2.2049 0.4535
Stomach-esophagus	0.1696	0.0300	5.6530 0.1769
Muscle-skeleton	0.0684	0.0753	0.9078 1.1016
Kidneys	0.0151	0.0607	0.2493 4.0107
Pancreas	0.0749	0.1066	0.7019 1.4246
Penis	0.0715	0.0106	6.7118 0.1490
Prostate	0.0611	0.0214	2.8624 0.3494
Uterus	0.0254		
Breast hyperplasia	0.0997		
Small intestine	0.0386		
Prostatic hyperplasia	0.0445		
Seminal vesicles	0.0941		
Sensory organs	0.0670		
White blood cells			

FETUS
% freq.

Development	0.0615
Gastrointestinal	0.0154
Brain	0.0000
Hematopoietic	0.0079
Heart-blood vessels	0.0041
Lungs	0.0074
Kidneys	0.0185
Prostate	0.0499
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0408
Ovary-uterus	0.0114
Endocrine tissue	0.0000
Fetal	0.0338
Gastrointestinal	0.1098
Hematopoietic	0.0114
Skin-muscle	0.0421
Testicles	0.0312
Lungs	0.2786
Nerves	0.0080
Prostate	0.0192
Sensory organs	0.0000

Electronic Northern Blot for SEQ. ID. NO: 64

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
Bladder	0.0093	0.0153	0.6062 1.6497
Breast	0.0160	0.0174	0.9174 1.0901
Ovary	0.0091	0.0182	0.5008 1.9967
Endocrine tissue	0.0201	0.0109	1.8419 0.5429
Gastrointestinal	0.0194	0.0333	0.5816 1.7193
Brain	0.0076	0.0219	0.3483 2.8707
Hematopoietic	0.0182	0.0378	0.4805 2.0811
Skin	0.0050	0.0000	undef 0.0000
Hepatic	0.0099	0.0323	0.3061 3.2673
Heart	0.0148	0.0275	0.5395 1.8535
Testicles	0.0122	0.0000	undef 0.0000
Lungs	0.0174	0.0118	1.4748 0.6781
Stomach-esophagus	0.0290	0.0307	0.9449 1.0583
Muscle-skeleton	0.0154	0.0120	1.2848 0.7783
Kidneys	0.0416	0.0068	6.0782 0.1645
Pancreas	0.0170	0.0110	1.5428 0.6482
Penis	0.0120	0.0267	0.4492 2.2260
Prostate	0.0191	0.0085	2.2373 0.4470
Uterus	0.0149	0.0142	1.0444 0.9575
Breast hyperplasia	0.0182		
Small intestine	0.0187		
Prostatic hyperplasia	0.0059		
Seminal vesicles	0.0178		
Sensory organs	0.0353		
White blood cells	0.0183		

FETUS
% freq.

Development	0.0307
Gastrointestinal	0.0062
Brain	0.0000
Hematopoietic	0.0393
Heart-blood vessels	0.0000
Lungs	0.0074
Kidneys	0.0124
Prostate	0.0249
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0476
Ovary-uterus	0.0571
Endocrine tissue	0.0245
Fetal	0.0175
Gastrointestinal	0.0244
Hematopoietic	0.0114
Skin-muscle	0.0291
Testicles	0.0000
Lungs	0.0082
Nerves	0.0020
Prostate	0.0000
Sensory organs	0.0310

Electronic Northern for Seq. ID: 217

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma	0.0100	0.0136	0.7358 1.3590
Bladder	0.0039	0.0094	0.4149 2.4102
Breast	0.0053	0.0028	1.8786 0.5323
Large intestine	0.0153	0.0028	5.3823 0.1858
Small intestine	0.0027	0.0000	undef 0.0000
Ovary	0.0030	0.0000	undef 0.0000
Endocrine tissue	0.0032	0.0114	0.2826 3.5381
Brain	0.0072	0.0060	1.2090 0.8271
Skin	0.0037	0.0000	undef 0.0000
Hepatic	0.0046	0.0127	0.3662 2.7307
Heart	0.0071	0.0137	0.5169 1.9348
Testicles	0.0080	0.0059	1.3570 0.7369
Lung	0.0107	0.0037	2.8941 0.3455
Stomach-esophagus	0.0000	0.0064	0.0000 undef
Muscle-skeleton	0.0086	0.0000	undef 0.0000
Kidney	0.0045	0.0048	0.9284 1.0771
Pancreas	0.0116	0.0055	2.0940 0.4776
Prostate	0.0038	0.0013	2.8940 0.3455
T lymphoma	0.0025	0.0075	0.3381 2.9576
Uterus	0.0031	0.0092	0.3368 2.9684
White blood cells	0.0089	0.0000	undef 0.0000
Hematopoietic	0.0067		
Penis	0.0054		
Seminal vesicle	0.0000		
Sensory organs	0.0000		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0028
Brain	0.0125
Hematopoietic	0.0079
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0071
Lung	0.0036
Adrenal gland	0.0000
Kidney	0.0124
Placenta	0.0121
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0204
Breast_t	0.0000
Large intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0152
Endocrine tissue	0.0000
Fetal	0.0046
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0130
Testicles_n	0.0167
Testicles_t	0.0000
Lungs_n	0.0000
Lungs_t	0.0000
Nerves	0.0070
Kidney_t	0.0000
Ovary uterus	0.0203
Prostate_n	0.0121
Sensory organs	0.0000
White blood cells	0.0000

Electronic Northern for Seq. ID: 218

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma	0.0075	0.0000	undef 0.0000
Bladder	0.0078	0.0117	0.6638 1.5064
Breast	0.0114	0.0169	0.6784 1.4741
Large intestine	0.0115	0.0085	1.3456 0.7432
Small intestine	0.0110	0.0107	1.0306 0.9703
Ovary	0.0059	0.0072	0.8295 1.2055
Endocrine tissue	0.0144	0.0038	3.8156 0.2621
Brain	0.0193	0.0110	1.7586 0.5686
Skin	0.0220	0.0000	undef 0.0000
Hepatic	0.0000	0.0190	0.0000 undef
Heart	0.0173	0.0137	1.2552 0.7967
Testicles	0.0080	0.0059	1.3570 0.7369
Lung	0.0165	0.0111	1.4909 0.6707
Stomach-esophagus	0.0000	0.0128	0.0000 undef
Muscle-skeleton	0.0051	0.0037	1.3917 0.7186
Kidney	0.0179	0.0048	3.7136 0.2693
Pancreas	0.0033	0.0442	0.0748 13.3714
Prostate	0.0085	0.0039	2.1705 0.4607
T lymphoma	0.0101	0.0075	1.3525 0.7394
Uterus	0.0093	0.0138	0.6735 1.4847
White blood cells	0.0096	0.0304	0.3156 3.1685
Hematopoietic	0.0094		
Penis	0.0134		
Seminal vesicle	0.0352		
Sensory organs	0.0000		
	FETUS % freq.		
	0.0000		
Development	0.0028		
Gastrointestinal	0.0188		
Brain	0.0079		
Hematopoietic	0.0000		
Skin	0.0000		
Hepatic	0.0000		
Heart-blood vessels	0.0145		
Lung	0.0000		
Adrenal gland	0.0185		
Kidney	0.0182		
Placenta	0.0000		
Prostate	0.0000		
Sensory organs	0.0000		

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0068
Breast_t	0.0000
Large intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0101
Endocrine tissue	0.0000
Fetal	0.0029
Gastrointestinal	0.0244
Hematopoietic	0.0513
Skin-muscle	0.0194
Testicles_n	0.0000
Testicles_t	0.0000
Lungs_n	0.0586
Lungs_t	0.0000
Nerve	0.0000
Kidney_t	0.0161
Ovary Uterus	0.0000
Prostate_n	0.0068
Sensory organs	0.0182
White blood cells	0.0077
	0.0000

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Electronic Northern for Seq. ID: 219

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma	0.0075	0.0000	undef 0.0000
Bladder	0.0156	0.0047	3.3190 0.3013
Breast	0.0185	0.0211	0.8767 1.1406
Large intestine	0.0307	0.0199	1.5378 0.6503
Small intestine	0.0082	0.0213	0.3865 2.5875
Ovary	0.0059	0.0334	0.1778 5.6255
Endocrine tissue	0.0305	0.0266	1.1468 0.8720
Brain	0.0393	0.0189	2.0767 0.4815
Skin	0.0257	0.0000	undef 0.0000
Hepatic	0.0000	0.0127	0.0000 undef
Heart	0.0447	0.0000	undef 0.0000
Testicles	0.0161	0.0118	1.3571 0.7369
Lung	0.0282	0.0240	1.1739 0.8519
Stomach-esophagus	0.0072	0.0000	undef 0.0000
Muscle-skeleton	0.0154	0.0074	2.0875 0.4750
Kidney	0.0269	0.0193	1.3927 0.7180
Pancreas	0.0066	0.0000	undef 0.0000
Prostate	0.0179	0.0065	2.7494 0.3637
T lymphoma	0.0177	0.0672	0.2630 3.8026
Uterus	0.0118	0.0046	2.5703 0.3891
White blood cells	0.0226	0.0000	undef 0.0000
Hematopoietic	0.0147		
Penis	0.0188		
Seminal vesicle	0.0281		
Sensory organs	0.0000		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0167
Brain	0.0188
Hematopoietic	0.0079
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0356
Lung	0.0145
Adrenal gland	0.0254
Kidney	0.0185
Placenta	0.0182
Prostate	0.0249
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0068
Breast_t	0.0000
Large intestine_t	0.0000
Ovary_n	0.1595
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0122
Gastrointestinal	0.0122
Hematopoietic	0.0000
Skin-muscle	0.0292
Testicles_n	0.0167
Testicles_t	0.0000
Lungs_n	0.0195
Lungs_t	0.0000
Nerves	0.0311
Kidney_t	0.0000
Ovary uterus	0.0090
Prostate_n	0.0061
Sensory organs	0.0310
White blood cells	0.0000

Electronic Northern for Seq. ID: 220

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma	0.0050	0.0000	undef 0.0000
Bladder	0.0078	0.0000	undef 0.0000
Breast	0.0088	0.0070	1.2524 0.7985
Large intestine	0.0153	0.0085	1.7941 0.5574
Small intestine	0.0192	0.0213	0.9018 1.1089
Ovary	0.0059	0.0262	0.2262 4.4200
Endocrine tissue	0.0337	0.0142	2.3766 0.4208
Brain	0.0156	0.0070	2.2381 0.4468
Skin	0.0073	0.0000	undef 0.0000
Hepatic	0.0093	0.0063	1.4649 0.6826
Heart	0.0183	0.0000	undef 0.0000
Testicles	0.0161	0.0059	2.7142 0.3684
Lung	0.0185	0.0111	1.6663 0.6001
Stomach-esophagus	0.0000	0.0000	undef undef
Muscle-skeleton	0.0051	0.0037	1.3917 0.7186
Kidney	0.0157	0.0048	3.2497 0.3077
Pancreas	0.0099	0.0055	1.7949 0.5571
Prostate	0.0160	0.0065	2.4600 0.4065
T lymphoma	0.0152	0.0299	0.5072 1.9717
Uterus	0.0089	0.0046	1.9277 0.5188
White blood cells	0.0164	0.0304	0.5410 1.8483
Hematopoietic	0.0040		
Penis	0.0080		
Seminal vesicle	0.0141		
Sensory organs	0.0118		

FETUS
% freq.

Development	0.0139
Gastrointestinal	0.0056
Brain	0.0063
Hematopoietic	0.0118
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0178
Lung	0.0072
Adrenal gland	0.0000
Kidney	0.0000
Placenta	0.0182
Prostate	0.0249
Sensory organs	0.0126

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Breast_t	0.0000
Large intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0101
Endocrine tissue	0.0000
Fetal	0.0058
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0194
Testicles_n	0.0084
Testicles_t	0.0000
Lungs_n	0.0195
Lungs_t	0.0000
Nerves	0.0090
Kidney_t	0.0000
Ovary uterus	0.0090
Prostate_n	0.0121
Sensory organs	0.0000
White blood cells	0.0000

Electronic Northern for Seq. ID: 221

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma	0.0100	0.0000	undef 0.0000
Bladder	0.0078	0.0047	1.6595 0.6026
Breast	0.0079	0.0056	1.4090 0.7097
Large intestine	0.0057	0.0085	0.6728 1.4864
Small intestine	0.0082	0.0000	undef 0.0000
Ovary	0.0030	0.0143	0.2074 4.8219
Endocrine tissue	0.0112	0.0106	1.0563 0.9467
Brain	0.0052	0.0040	1.3056 0.7659
Skin	0.0037	0.0000	undef 0.0000
Hepatic	0.0000	0.0063	0.0000 undef
Heart	0.0132	0.0000	undef 0.0000
Testicles	0.0040	0.0000	undef 0.0000
Lung	0.0117	0.0129	0.9021 1.1085
Stomach-esophagus	0.0000	0.0064	0.0000 undef
Muscle-skeleton	0.0086	0.0074	1.1597 0.8623
Kidney	0.0179	0.0048	3.7139 0.2693
Pancreas	0.0093	0.0000	undef 0.0000
Prostate	0.0113	0.0065	1.7364 0.5759
T lymphoma	0.0000	0.0149	0.0000 undef
Uterus	0.0044	0.0046	0.9638 1.0375
White blood cells	0.0075	0.0304	0.2480 4.0326
Hematopoietic	0.0067		
Penis	0.0080		
Seminal vesicle	0.0141		
Sensory organs	0.0118		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0028
Brain	0.0063
Hematopoietic	0.0039
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0000
Adrenal gland	0.0000
Kidney	0.0062
Placenta	0.0242
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Breast_t	0.0000
Large intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0023
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0065
Testicles_n	0.0042
Testicles_t	0.0000
Lungs_n	0.0195
Lungs_t	0.0000
Nerves	0.0050
Kidney_t	0.0000
Ovary uterus	0.0000
Prostate_n	0.0121
Sensory organs	0.0774
White blood cells	0.0000

Electronic Northern for Seq. ID: 222

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma	0.0000	0.0000	undef undef
Bladder	0.0351	0.0047	7.4677 0.1339
Breast	0.0070	0.0014	5.0097 0.1996
Large intestine	0.0115	0.0000	undef 0.0000
Small intestine	0.0000	0.0000	undef undef
Ovary	0.0000	0.0024	0.0000 undef
Endocrine tissue	0.0016	0.0035	0.4527 2.2091
Brain	0.0017	0.0060	0.2901 3.4467
Skin	0.0000	0.0000	undef undef
Hepatic	0.0000	0.0063	0.0000 undef
Heart	0.0000	0.0137	0.1477 6.7715
Testicles	0.0040	0.0000	undef 0.0000
Lung	0.0039	0.0018	2.1049 0.4751
Stomach-esophagus	0.0145	0.0000	undef 0.0000
Muscle-skeleton	0.0051	0.0000	undef 0.0000
Kidney	0.0112	0.0000	undef 0.0000
Pancreas	0.0017	0.0055	0.2992 3.3427
Prostate	0.0075	0.0026	2.8941 0.3455
T lymphoma	0.0025	0.0000	undef 0.0000
Uterus	0.0059	0.0046	1.2851 0.7781
White blood cells	0.0027	0.0000	undef 0.0000
Hematopoietic	0.0013		
Penis	0.0054		
Seminal vesicle	0.0000		
Sensory organs	0.0000		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0039
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0000
Adrenal gland	0.0254
Kidney	0.0185
Placenta	0.0121
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0340
Breast_t	0.0000
Large Intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0017
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0065
Testicles_n	0.0000
Testicles_t	0.0000
Lungs_n	0.0098
Lungs_t	0.0000
Nerves	0.0020
Kidney_t	0.0000
Ovary uterus	0.0000
Prostate_n	0.0061
Sensory organs	0.0000
White blood cells	0.0000

Electronic Northern for Seq. ID: 223

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma	0.0100	0.0000	undef 0.0000
Bladder	0.0273	0.0117	2.3233 0.4304
Breast	0.0150	0.0098	1.5208 0.6576
Large intestine	0.0077	0.0028	2.6911 0.3716
Small intestine	0.0110	0.0000	undef 0.0000
Ovary	0.0089	0.0024	3.7330 0.2679
Endocrine tissue	0.0016	0.0053	0.3018 3.3136
Brain	0.0069	0.0100	0.6963 1.4361
Skin	0.0037	0.0000	undef 0.0000
Hepatic	0.0000	0.0190	0.0000 undef
Heart	0.0081	0.0137	0.5907 1.6929
Testicles	0.0040	0.0000	undef 0.0000
Lung	0.0068	0.0111	0.6139 1.6289
Stomach-esophagus	0.0072	0.0128	0.5668 1.7644
Muscle-skeleton	0.0086	0.0037	2.3194 0.4311
Kidney	0.0112	0.0000	undef 0.0000
Pancreas	0.0050	0.0055	0.8975 1.1142
Prostate	0.0141	0.0169	0.8348 1.1978
T lymphoma	0.0202	0.0075	2.7049 0.3697
Uterus	0.0177	0.0000	undef 0.0000
White blood cells	0.0096	0.0000	undef 0.0000
Hematopoietic	0.0187		
Penis	0.0080		
Seminal vesicle	0.0281		
Sensory organs	0.0000		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0056
Brain	0.0000
Hematopoietic	0.0157
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0071
Lung	0.0145
Adrenal gland	0.0000
Kidney	0.0062
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0068
Breast_t	0.0000
Large intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0046
Gastrointestinal	0.0122
Hematopoietic	0.0000
Skin	0.0000
Testicles_n	0.0000
Testicles_t	0.0000
Lungs_n	0.0098
Lungs_t	0.0000
Nerves	0.0010
Kidney_t	0.0000
Ovary_uterus	0.0023
Prostate_n	0.0121
Sensory organs	0.0155
White blood cells	0.0000

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Electronic Northern for Seq. ID: 224

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma	0.0050	0.0000	undef 0.0000
Bladder	0.0078	0.0000	undef 0.0000
Breast	0.0018	0.0112	0.1566 6.3876
Large intestine	0.0057	0.0057	1.0092 0.9909
Small intestine	0.0027	0.0000	undef 0.0000
Ovary	0.0059	0.0143	0.4148 2.4109
Endocrine tissue	0.0032	0.0053	0.6036 1.6568
Brain	0.0029	0.0060	0.4835 2.0680
Skin	0.0000	0.0000	undef undef
Hepatic	0.0093	0.0000	undef 0.0000
Heart	0.0051	0.0000	undef 0.0000
Testicles	0.0000	0.0000	undef undef
Lung	0.0039	0.0037	1.0524 0.9502
Stomach-esophagus	0.0072	0.0000	undef 0.0000
Muscle-skeleton	0.0017	0.0037	0.4639 2.1557
Kidney	0.0112	0.0048	2.3212 0.4308
Pancreas	0.0099	0.0055	1.7949 0.5571
Prostate	0.0066	0.0063	1.0129 0.9872
T lymphoma	0.0025	0.0000	undef 0.0000
Uterus	0.0000	0.0000	undef undef
White blood cells	0.0034	0.0000	undef 0.0000
Hematopoietic	0.0053		
Penis	0.0080		
Seminal vesicle	0.0000		
Sensory organs	0.0000		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0056
Brain	0.0000
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0260
Heart-blood vessels	0.0107
Lung	0.0000
Adrenal gland	0.0000
Kidney	0.0000
Placenta	0.0061
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Breast_t	0.0000
Large Intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0000
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles_n	0.0000
Testicles_t	0.0000
Lungs_n	0.0000
Lungs_t	0.0098
Nerves	0.0000
Kidney_t	0.0030
Ovary uterus	0.0000
Prostate_n	0.0000
Sensory organs	0.0243
White blood cells	0.0000
	0.0000

Electronic Northern for Seq. ID: 225

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma	0.0075	0.0136	0.5519 1.8120
Bladder	0.0078	0.0023	3.3190 0.3013
Breast	0.0053	0.0056	0.9393 1.0646
Large intestine	0.0057	0.0000	undef 0.0000
Small intestine	0.0027	0.0000	undef 0.0000
Ovary	0.0059	0.0072	0.8296 1.2055
Endocrine tissue	0.0177	0.0018	9.9589 0.1004
Brain	0.0075	0.0050	1.5087 0.6628
Skin	0.0000	0.0000	undef undef
Hepatic	0.0000	0.0127	0.0000 undef
Heart	0.0061	0.0000	undef 0.0000
Testicles	0.0161	0.0000	undef 0.0000
Lung	0.0088	0.0111	0.7893 1.2669
Stomach-esophagus	0.0000	0.0064	0.0000 undef
Muscle-skeleton	0.0034	0.0074	0.4639 2.1557
Kidney	0.0090	0.0048	1.8570 0.5385
Pancreas	0.0099	0.0055	1.7949 0.5571
Prostate	0.0113	0.0013	8.6822 0.1152
T lymphoma	0.0025	0.0075	0.3381 2.9576
Uterus	0.0059	0.0046	1.2851 0.7781
White blood cells	0.0034	0.0000	undef 0.0000
Hematopoietic	0.0053		
Penis	0.0080		
Seminal vesicle	0.0000		
Sensory organs	0.0000		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0111
Brain	0.0000
Hematopoietic	0.0039
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0000
Adrenal gland	0.0000
Kidney	0.0000
Placenta	0.0182
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0068
Breast_t	0.0000
Large intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0127
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0032
Testicles_n	0.0167
Testicles_t	0.0000
Lungs_n	0.0000
Lungs_t	0.0000
Nerves	0.0000
Kidney_t	0.0040
Ovary uterus	0.0000
Prostate_n	0.0180
Sensory organs	0.0061
White blood cells	0.0000
	0.0000

Electronic Northern for Seq. ID: 226

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma	0.0000	0.0000	undef undef
Bladder	0.0000	0.0023	0.0000 undef
Breast	0.0053	0.0056	0.9393 1.0646
Large intestine	0.0057	0.0000	undef 0.0000
Small intestine	0.0000	0.0000	undef undef
Ovary	0.0000	0.0000	undef undef
Endocrine tissue	0.0016	0.0053	0.3018 3.3136
Brain	0.0035	0.0020	1.7408 0.5745
Skin	0.0000	0.0000	undef undef
Hepatic	0.0046	0.0000	undef 0.0000
Heart	0.0010	0.0000	undef 0.0000
Testicles	0.0000	0.0059	0.0000 undef
Lung	0.0019	0.0000	undef 0.0000
Stomach-esophagus	0.0000	0.0000	undef undef
Muscle-skeleton	0.0017	0.0000	undef 0.0000
Kidney	0.0045	0.0048	0.9285 1.0770
Pancreas	0.0033	0.0000	undef 0.0000
Prostate	0.0038	0.0000	undef 0.0000
T lymphoma	0.0000	0.0000	undef undef
Uterus	0.0059	0.0046	1.2851 0.7791
White blood cells	0.0027	0.0000	undef 0.0000
Hematopoietic	0.0000	0.0080	0.0000
Penis	0.0000	0.0000	0.0000
Seminal vesicle	0.0000	0.0000	0.0000
Sensory organs	0.0000	0.0000	0.0000

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0125
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0036
Lung	0.0036
Adrenal gland	0.0000
Kidney	0.0062
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Breast_t	0.0000
Large intestine_t	0.0000
Ovary_n	0.1595
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0046
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0097
Testicles_n	0.0000
Testicles_t	0.0000
Lungs_n	0.0000
Lungs_t	0.0000
Nerves	0.0070
Kidney_t	0.0000
Ovary uterus	0.0023
Prostate_n	0.0182
Sensory organs	0.0077
White blood cells	0.0000

Electronic Northern for Seq. ID: 227

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma	0.0038	0.0000	undef 0.0000
Bladder	0.0000	0.0094	0.0000 undef
Breast	0.0025	0.0089	0.2793 3.5727
Large intestine	0.0057	0.0228	0.2523 3.9638
Small intestine	0.0082	0.0000	undef 0.0000
Ovary	0.0059	0.0095	0.6222 1.6073
Endocrine tissue	0.0096	0.0033	2.9275 0.3416
Brain	0.0134	0.0050	2.6904 0.3717
Skin	0.0037	0.0000	undef 0.0000
Hepatic	0.0093	0.0063	1.4649 0.6826
Heart	0.0081	0.0137	0.5907 1.6928
Testicles	0.0161	0.0000	undef 0.0000
Lung	0.0049	0.0037	1.3158 0.7600
Stomach-esophagus	0.0000	0.0165	0.0000 undef
Muscle-skeleton	0.0000	0.0074	0.0000 undef
Kidney	0.0112	0.0000	undef 0.0000
Pancreas	0.0033	0.0092	0.3604 2.7748
Prostate	0.0113	0.0078	1.4470 0.6911
T lymphoma	0.0033	0.0173	0.1901 5.2613
Uterus	0.0118	0.0046	2.5702 0.3891
White blood cells	0.0023	0.0000	undef 0.0000
Hematopoietic	0.0047		
Penis	0.0027		
Seminal vesicle	0.0000		
Sensory organs	0.0118		

FETUS
% freq.

Development	0.0278
Gastrointestinal	0.0111
Brain	0.0000
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0036
Heart-blood vessels	0.0108
Lung	0.0000
Adrenal gland	0.0000
Kidney	0.0000
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0126

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0068
Breast_t	0.0000
Large_intestine_t	0.0125
Ovary_t	0.0379
Endocrine tissue	0.0000
Fetal	0.0066
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0090
Testicles_n	0.0000
Testicles_t	0.0169
Lungs_n	0.0228
Lungs_t	0.0000
Nerves	0.0000
Kidney_t	0.0191
Ovary_uterus	0.0495
Prostate_n	0.0325
Sensory Organs	0.0182
	0.0077

Electronic Northern for Seq. ID: 228

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma	0.0025	0.0000	undef 0.0000
Bladder	0.0000	0.0094	0.0000 undef
Breast	0.0070	0.0056	1.2524 0.7985
Large intestine	0.0057	0.0000	undef 0.0000
Small intestine	0.0055	0.0000	undef 0.0000
Ovary	0.0148	0.0048	3.1108 0.3215
Endocrine tissue	0.0016	0.0018	0.9054 1.1045
Brain	0.0064	0.0060	1.0638 0.9400
Skin	0.0110	0.0000	undef 0.0000
Hepatic	0.0000	0.0127	0.0000 undef
Heart	0.0030	0.0000	undef 0.0000
Testicles	0.0080	0.0118	0.6786 1.4737
Lung	0.0019	0.0074	0.2631 3.9007
Stomach-esophagus	0.0145	0.0000	undef 0.0000
Muscle-skeleton	0.0034	0.0000	undef 0.0000
Kidney	0.0045	0.0000	undef 0.0000
Pancreas	0.0017	0.0000	undef 0.0000
Prostate	0.0057	0.0026	2.1706 0.4607
T lymphoma	0.0025	0.0000	undef 0.0000
Uterus	0.0015	0.0046	0.3213 3.1125
White blood cells	0.0048	0.0000	undef 0.0000
Hematopoietic	0.0067		
Penis	0.0027		
Seminal vesicle	0.0070		
Sensory organs	0.0118		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0111
Brain	0.0000
Hematopoietic	0.0039
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0072
Adrenal gland	0.0000
Kidney	0.0000
Placenta	0.0121
Prostate	0.0249
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0136
Breast_t	0.0000
Large intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0245
Fetal	0.0017
Gastrointestinal	0.0122
Hematopoietic	0.0000
Skin-muscle	0.0032
Testicles_n	0.0042
Testicles_t	0.0000
Lungs_n	0.0098
Lungs_t	0.0000
Nerves	0.0060
Kidney_t	0.0000
Ovary uterus	0.0023
Prostate_n	0.0182
Sensory organs	0.0000
White blood cells	0.0000

Electronic Northern for Seq. ID: 229

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma	0.0000	0.0000	undef undef
Bladder	0.0039	0.0023	1.6595 0.6026
Breast	0.0018	0.0000	undef 0.0000
Large intestine	0.0019	0.0028	0.6728 1.4864
Small intestine	0.0027	0.0000	undef 0.0000
Ovary	0.0000	0.0000	undef undef
Endocrine tissue	0.0016	0.0000	undef 0.0000
Brain	0.0000	0.0020	0.0000 undef
Skin	0.0000	0.0000	undef undef
Hepatic	0.0000	0.0000	undef undef
Heart	0.0000	0.0000	undef undef
Testicles	0.0000	0.0000	undef undef
Lung	0.0000	0.0059	0.0000 undef
Stomach-esophagus	0.0010	0.0018	0.5262 1.9004
Muscle-skeleton	0.0000	0.0000	undef undef
Kidney	0.0017	0.0037	0.4639 2.1557
Pancreas	0.0000	0.0000	undef undef
Prostate	0.0017	0.0000	undef 0.0000
T lymphoma	0.0038	0.0000	undef 0.0000
Uterus	0.0000	0.0000	undef undef
White blood cells	0.0000	0.0000	undef undef
Hematopoietic	0.0007	0.0000	undef 0.0000
Penis	0.0000		
Seminal vesicle	0.0027		
Sensory organs	0.0000		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0036
Adrenal gland	0.0000
Kidney	0.0000
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Breast_t	0.0000
Large intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0035
Gastrointestinal	0.0122
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles_n	0.0000
Testicles_t	0.0000
Lungs_n	0.0000
Lungs_t	0.0000
Nerves	0.0000
Kidney_t	0.0000
Ovary Uterus	0.0000
Prostate_n	0.0121
Sensory organs	0.0000
White blood cells	0.0000

Electronic Northern for Seq. ID: 230

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma	0.0050	0.0136	0.3679 2.7181
Bladder	0.0000	0.0023	0.0000 undef
Breast	0.0053	0.0042	1.2524 0.7985
Large intestine	0.0038	0.0057	0.6728 1.4864
Small intestine	0.0055	0.0000	undef 0.0000
Ovary	0.0148	0.0072	2.0739 0.4822
Endocrine tissue	0.0080	0.0106	0.7545 1.3254
Brain	0.0046	0.0060	0.7737 1.2925
Skin	0.0000	0.0000	undef undef
Hepatic	0.0093	0.0000	undef 0.0000
Heart	0.0041	0.0000	undef 0.0000
Testicles	0.0120	0.0000	undef 0.0000
Lung	0.0010	0.0018	0.5262 1.9004
Stomach-esophagus	0.0000	0.0000	undef undef
Muscle-skeleton	0.0086	0.0185	0.4639 2.1557
Kidney	0.0022	0.0048	0.4642 2.1540
Pancreas	0.0017	0.0000	undef 0.0000
Prostate	0.0019	0.0013	1.4470 0.6911
T lymphoma	0.0000	0.0075	0.0000 undef
Uterus	0.0015	0.0230	0.0643 15.5627
White blood cells	0.0014	0.0000	undef 0.0000
Hematopoietic	0.0027		
Penis	0.0027		
Seminal vesicle	0.0000		
Sensory organs	0.0000		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0139
Brain	0.0188
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0000
Adrenal gland	0.0000
Kidney	0.0062
Placenta	0.0061
Prostate	0.0000
Sensory organs	0.0126

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Breast_t	0.0000
Large intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0151
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0130
Testicles_n	0.0376
Testicles_t	0.0000
Lungs_n	0.0098
Lungs_t	0.0000
Nerves	0.0100
Kidney_t	0.0000
Ovary Uterus	0.0045
Prostate_n	0.0182
Sensory organs	0.0310
White blood cells	0.0000

Electronic Northern for Seq. ID: 231

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma	0.0000	0.0136	0.0000 undef
Bladder	0.0117	0.0047	2.4892 0.4017
Breast	0.0053	0.0028	1.8786 0.5323
Large intestine	0.0038	0.0000	undef 0.0000
Small intestine	0.0110	0.0213	0.5153 1.9406
Ovary	0.0030	0.0072	0.4148 2.4109
Endocrine tissue	0.0064	0.0053	1.2071 0.8284
Brain	0.0064	0.0140	0.4559 2.1934
Skin	0.0110	0.0000	undef 0.0000
Hepatic	0.0000	0.0254	0.0000 undef
Heart	0.0000	0.0137	0.0000 undef
Testicles	0.0000	0.0059	0.0000 undef
Lung	0.0068	0.0055	1.2278 0.8144
Stomach-esophagus	0.0000	0.0000	undef undef
Muscle-skeleton	0.0000	0.0000	undef undef
Kidney	0.0067	0.0096	0.6964 1.4360
Pancreas	0.0017	0.0000	undef 0.0000
Prostate	0.0104	0.0039	2.6529 0.3769
T lymphoma	0.0025	0.0075	0.3381 2.9576
Uterus	0.0044	0.0000	undef 0.0000
White blood cells	0.0027	0.0000	undef 0.0000
Hematopoietic	0.0013		
Penis	0.0080		
Seminal vesicle	0.0070		
Sensory organs	0.0000		
	FETUS % freq.		

Development	0.0418
Gastrointestinal	0.0000
Brain	0.0125
Hematopoietic	0.0039
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0071
Lung	0.0000
Adrenal gland	0.0000
Kidney	0.0062
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Breast_t	0.0000
Large intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0051
Endocrine tissue	0.0000
Fetal	0.0017
Gastrointestinal	0.0244
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles_n	0.0000
Testicles_t	0.0000
Lungs_n	0.0098
Lungs_t	0.0000
Nerves	0.0030
Kidney_t	0.0000
Ovary uterus	0.0023
Prostate_n	0.0061
Sensory organs	0.0000
White blood cells	0.0000

Electronic Northern for Seq. ID: 232

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma	0.0100	0.0136	0.7358 1.3590
Bladder	0.0117	0.0094	1.2446 0.8035
Breast	0.0150	0.0056	2.6614 0.3757
Large intestine	0.0038	0.0199	0.1922 5.2023
Small intestine	0.0110	0.0000	undef 0.0000
Ovary	0.0119	0.0215	0.5530 1.8082
Endocrine tissue	0.0048	0.0053	0.9054 1.1045
Brain	0.0046	0.0040	1.1605 0.8617
Skin	0.0037	0.0000	undef 0.0000
Hepatic	0.0046	0.0190	0.2441 4.0959
Heart	0.0142	0.0137	1.0337 0.9674
Testicles	0.0080	0.0118	0.6786 1.4737
Lung	0.0078	0.0092	0.8419 1.1677
Stomach-esophagus	0.0000	0.0064	0.0000 undef
Muscle-skeleton	0.0034	0.0074	0.4639 2.1557
Kidney	0.0067	0.0096	0.6964 1.4360
Pancreas	0.0066	0.0000	undef 0.0000
Prostate	0.0123	0.0039	3.1353 0.3190
T lymphoma	0.0101	0.0224	0.4508 2.2182
Uterus	0.0044	0.0046	0.9638 1.0375
White blood cells	0.0062	0.0000	undef 0.0000
Hematopoietic	0.0134		
Penis	0.0134		
Seminal vesicle	0.0000		
Sensory organs	0.0118		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0139
Brain	0.0000
Hematopoietic	0.0157
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0107
Lung	0.0181
Adrenal gland	0.0254
Kidney	0.0000
Placenta	0.0121
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Breast t	0.0000
Large intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0152
Endocrine tissue	0.0245
Fetal	0.0087
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0065
Testicles_n	0.0376
Testicles_t	0.0000
Lungs_n	0.0293
Lungs_t	0.0000
Nerves	0.0100
Kidney t	0.0000
Ovary uterus	0.0338
Prostate n	0.0061
Sensory organs	0.0000
White blood cells	0.0000

Electronic Northern for Seq. ID: 233

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma	0.0050	0.0000	undef 0.0000
Bladder	0.0078	0.0117	0.6638 1.5065
Breast	0.0088	0.0155	0.5693 1.7566
Large intestine	0.0211	0.0028	7.4006 0.1351
Small intestine	0.0027	0.0000	undef 0.0000
Ovary	0.0149	0.0024	4.9773 0.2009
Endocrine tissue	0.0032	0.0142	0.2263 4.4181
Brain	0.0035	0.0000	undef 0.0000
Skin	0.0257	0.0000	undef 0.0000
Hepatic	0.0279	0.0000	undef 0.0000
Heart	0.0071	0.0137	0.5169 1.9347
Testicles	0.0040	0.0000	undef 0.0000
Lung	0.0292	0.0146	1.9733 0.5068
Stomach-esophagus	0.0000	0.0064	0.0000 undef
Muscle-skeleton	0.0017	0.0000	undef 0.0000
Kidney	0.0269	0.0000	undef 0.0000
Pancreas	0.0165	0.0000	undef 0.0000
Prostate	0.0141	0.0052	2.7132 0.3686
T lymphoma	0.0000	0.0000	undef undef
Uterus	0.0044	0.0000	undef 0.0000
White blood cells	0.0000	0.0000	undef undef
Hematopoietic	0.0040	0.0000	undef undef
Penis	0.0000		
Seminal vesicle	0.0070		
Sensory organs	0.0000		
	0.0000		
	FETUS		
	% freq.		
	0.0000		
Development	0.0056		
Gastrointestinal	0.0000		
Brain	0.0039		
Hematopoietic	0.0000		
Skin	0.0000		
Hepatic	0.0036		
Heart-blood vessels	0.0145		
Lung	0.0254		
Adrenal gland	0.0000		
Kidney	0.0000		
Placenta	0.0000		
Prostate	0.0000		
Sensory organs	0.0000		

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Breast_t	0.0000
Large intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0058
Gastrointestinal	0.0244
Hematopoietic	0.0000
Skin-muscle	0.0130
Testicles_n	0.0000
Testicles_t	0.0000
Lungs_n	0.0293
Lungs_t	0.0000
Nerves	0.0020
Kidney_t	0.0000
Ovary Uterus	0.0068
Prostate_n	0.0243
Sensory organs	0.0000
White blood cells	0.0000

Electronic Northern for Seq. ID: 234

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma	0.0025	0.0000	undef 0.0000
Bladder	0.0000	0.0094	0.0000 undef
Breast	0.0035	0.0056	0.6262 1.5969
Large intestine	0.0038	0.0000	undef 0.0000
Small intestine	0.0027	0.0000	undef 0.0000
Ovary	0.0059	0.0000	undef 0.0000
Endocrine tissue	0.0048	0.0018	2.7161 0.3682
Brain	0.0035	0.0010	3.4816 0.2872
Skin	0.0000	0.0000	undef undef
Hepatic	0.0000	0.0063	0.0000 undef
Heart	0.0020	0.0000	undef 0.0000
Testicles	0.0040	0.0000	undef 0.0000
Lung	0.0049	0.0000	undef 0.0000
Stomach-esophagus	0.0072	0.0000	undef 0.0000
Muscle-skeleton	0.0017	0.0037	0.4639 2.1557
Kidney	0.0022	0.0000	undef 0.0000
Pancreas	0.0017	0.0000	undef 0.0000
Prostate	0.0038	0.0000	undef 0.0000
T lymphoma	0.0126	0.0046	1.6064 0.6225
Uterus	0.0074	0.0304	0.1803 5.5448
White blood cells	0.0013		
Hematopoietic	0.0000		
Penis	0.0141		
Seminal vesicle	0.0000		
Sensory organs	0.0000		

FETUS
% freq.

Development	0.0139
Gastrointestinal	0.0139
Brain	0.0063
Hematopoietic	0.0039
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0036
Adrenal gland	0.0000
Kidney	0.0124
Placenta	0.0061
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Breast_t	0.0000
Large intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0253
Endocrine tissue	0.0000
Fetal	0.0029
Gastrointestinal	0.0122
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles_n	0.0042
Testicles_t	0.0000
Lungs_n	0.0000
Lungs_t	0.0000
Nerves	0.0090
Kidney_t	0.0000
Ovary uterus	0.0113
Prostate_n	0.0061
Sensory organs	0.0000
White blood cells	0.0000

Electronic Northern for Seq. ID: 235

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma	0.0000	0.0136	0.0000 undef
Bladder	0.0000	0.0000	undef undef
Breast	0.0000	0.0014	0.0000 undef
Large intestine	0.0000	0.0000	undef undef
Small intestine	0.0000	0.0107	0.0000 undef
Ovary	0.0059	0.0048	1.2443 0.8036
Endocrine tissue	0.0016	0.0053	0.3018 3.3136
Brain	0.0006	0.0030	0.1934 5.1701
Skin	0.0037	0.0000	undef 0.0000
Hepatic	0.0000	0.0000	undef undef
Heart	0.0010	0.0000	undef 0.0000
Testicles	0.0080	0.0000	undef 0.0000
Lung	0.0019	0.0000	undef 0.0000
Stomach-esophagus	0.0000	0.0000	undef undef
Muscle-skeleton	0.0000	0.0000	undef undef
Kidney	0.0000	0.0000	undef undef
Pancreas	0.0000	0.0000	undef undef
Prostate	0.0000	0.0000	undef undef
T lymphoma	0.0038	0.0000	undef 0.0000
Uterus	0.0000	0.0000	undef undef
White blood cells	0.0000	0.0046	0.0000 undef
Hematopoietic	0.0007	0.0000	undef 0.0000
Penis	0.0000		
Seminal vesicle	0.0000		
Sensory organs	0.0000		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0063
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0072
Adrenal gland	0.0000
Kidney	0.0042
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Breast_t	0.0000
Large intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0017
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles_n	0.0042
Testicles_t	0.0000
Lungs_n	0.0135
Lungs_t	0.0000
Nerves	0.0010
Kidney_t	0.0000
Ovary Uterus	0.0023
Prostate_n	0.0182
Sensory organs	0.0000
White blood cells	0.0000

Electronic Northern for Seq. ID: 236

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma	0.0100	0.0000	undef 0.0000
Bladder	0.0000	0.0000	undef undef
Breast	0.0194	0.0084	2.2961 0.4355
Large intestine	0.0096	0.0000	undef 0.0000
Small intestine	0.0055	0.0000	undef 0.0000
Ovary	0.0059	0.0024	2.4887 0.4018
Endocrine tissue	0.0128	0.0053	2.4143 0.4142
Brain	0.0041	0.0070	0.5903 1.7234
Skin	0.0037	0.0000	undef 0.0000
Hepatic	0.0000	0.0000	undef undef
Heart	0.0051	0.0000	undef 0.0000
Testicles	0.0000	0.0000	undef undef
Lung	0.0058	0.0092	0.6315 1.5836
Stomach-esophagus	0.0000	0.0000	undef undef
Muscle-skeleton	0.0051	0.0037	1.3917 0.7186
Kidney	0.0090	0.0000	undef 0.0000
Pancreas	0.0050	0.0000	undef 0.0000
Prostate	0.0104	0.0039	2.6529 0.3769
T lymphoma	0.0025	0.0075	0.3381 2.9576
Uterus	0.0118	0.0000	undef 0.0000
White blood cells	0.0089	0.0000	undef 0.0000
Hematopoietic	0.0134		
Penis	0.0080		
Seminal vesicle	0.0000		
Sensory organs	0.0000		

FETUS
% freq.

Development	0.0056
Gastrointestinal	0.0000
Brain	0.0118
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0036
Heart-blood vessels	0.0000
Lung	0.0000
Adrenal gland	0.0000
Kidney	0.0242
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Breast_t	0.0000
Large intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0093
Fetal	0.0000
Gastrointestinal	0.0000
Hematopoietic	0.0065
Skin-muscle	0.0000
Testicles_n	0.0000
Testicles_t	0.0000
Lungs_n	0.0000
Lungs_t	0.0000
Nerves	0.0060
Kidney_t	0.0000
Ovary Uterus	0.0045
Prostate_n	0.0182
Sensory organs	0.0000
White blood cells	0.0000

Electronic Northern for Seq. ID: 238

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma	0.0075	0.0000	undef 0.0000
Bladder	0.0000	0.0047	0.0000 undef
Breast	0.0009	0.0014	0.6262 1.5969
Large intestine	0.0019	0.0028	0.6728 1.4864
Small intestine	0.0000	0.0000	undef undef
Ovary	0.0148	0.0024	6.2217 0.1607
Endocrine tissue	0.0016	0.0018	0.9054 1.1045
Brain	0.0017	0.0050	0.2901 3.4467
Skin	0.0037	0.0789	0.0466 21.4787
Hepatic	0.0000	0.0000	undef undef
Heart	0.0051	0.0000	undef 0.0000
Testicles	0.0120	0.0118	1.0178 0.9825
Lung	0.0029	0.0018	1.5786 0.6335
Stomach-esophagus	0.0072	0.0000	undef 0.0000
Muscle-skeleton	0.0017	0.0000	undef 0.0000
Kidney	0.0000	0.0000	undef undef
Pancreas	0.0017	0.0000	undef 0.0000
Prostate	0.0113	0.0026	4.3411 0.2304
T lymphoma	0.0025	0.0000	undef 0.0000
Uterus	0.0030	0.0092	0.3213 3.1125
White blood cells	0.0027	0.0000	undef 0.0000
Hematopoietic	0.0040		
Penis	0.0027		
Seminal vesicle	0.0070		
Sensory organs	0.0000		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0056
Brain	0.0000
Hematopoietic	0.0157
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0036
Adrenal gland	0.0000
Kidney	0.0000
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Breast_t	0.0000
Large intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0152
Endocrine tissue	0.0000
Fetal	0.0006
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles_n	0.0042
Testicles_t	0.0000
Lungs_n	0.0000
Lungs_t	0.0000
Nerves	0.0060
Kidney_t	0.0000
Ovary Uterus	0.0068
Prostate_n	0.0061
Sensory organs	0.0000
White blood cells	0.0000

Electronic Northern for Seq. ID: 239

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma	0.0125	0.0000	undef 0.0000
Bladder	0.0156	0.0094	1.6595 0.6026
Breast	0.0141	0.0225	0.6262 1.5969
Large intestine	0.0172	0.0085	2.0184 0.4955
Small intestine	0.0192	0.0213	0.9018 1.1089
Ovary	0.0237	0.0262	0.9050 1.1050
Endocrine tissue	0.0144	0.0160	0.9054 1.1045
Brain	0.0197	0.0269	0.7307 1.3686
Skin	0.0184	0.0000	undef 0.0000
Hepatic	0.0279	0.0190	1.4649 0.6826
Heart	0.0203	0.0275	0.7384 1.3543
Testicles	0.0040	0.0059	0.6786 1.4737
Lung	0.0175	0.0166	1.0524 0.9502
Stomach-esophagus	0.0217	0.0000	undef 0.0000
Muscle-skeleton	0.0103	0.0037	2.7833 0.3593
Kidney	0.0112	0.0289	0.3869 2.5849
Pancreas	0.0116	0.0055	2.0941 0.4775
Prostate	0.0141	0.0039	3.6176 0.2764
T lymphoma	0.0025	0.0075	0.3381 2.9576
Uterus	0.0148	0.0184	0.8032 1.2450
White blood cells	0.0068	0.0000	undef 0.0000
Hematopoietic	0.0040		
Penis	0.0134		
Seminal vesicle	0.0070		
Sensory organs	0.0235		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0167
Brain	0.0125
Hematopoietic	0.0157
Skin	0.0000
Hepatic	0.0260
Heart-blood vessels	0.0213
Lung	0.0072
Adrenal gland	0.0000
Kidney	0.0062
Placenta	0.0061
Prostate	0.0000
Sensory organs	0.0126

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Breast_t	0.0000
Large intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0245
Fetal	0.0168
Gastrointestinal	0.0122
Hematopoietic	0.0000
Skin-muscle	0.0227
Testicles_n	0.0125
Testicles_t	0.0000
Lungs_n	0.0098
Lungs_t	0.0000
Nerves	0.0261
Kidney_t	0.0000
Ovary uterus	0.0068
Prostate_n	0.0243
Sensory organs	0.0000
White blood cells	0.0000

Electronic Northern for Seq. ID: 240

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma	0.0025	0.0000	undef 0.0000
Bladder	0.0000	0.0023	0.0000 undef
Breast	0.0035	0.0014	2.5048 0.3992
Large intestine	0.0019	0.0000	undef 0.0000
Small intestine	0.0000	0.0000	undef undef
Ovary	0.0000	0.0000	undef undef
Endocrine tissue	0.0000	0.0024	0.0000 undef
Brain	0.0000	0.0000	undef undef
Skin	0.0041	0.0020	2.0309 0.4924
Hepatic	0.0000	0.0000	undef undef
Heart	0.0000	0.0000	undef undef
Testicles	0.0010	0.0137	0.0738 13.5431
Lung	0.0000	0.0000	undef undef
Stomach-esophagus	0.0000	0.0000	undef undef
Muscle-skeleton	0.0000	0.0000	undef undef
Kidney	0.0034	0.0037	0.9276 1.0778
Pancreas	0.0022	0.0000	undef 0.0000
Prostate	0.0000	0.0000	undef undef
T lymphoma	0.0057	0.0039	1.4470 0.6911
Uterus	0.0126	0.0000	undef 0.0000
White blood cells	0.0015	0.0000	undef 0.0000
Hematopoietic	0.0062	0.0000	undef 0.0000
Penis	0.0027	0.0000	undef 0.0000
Seminal vesicle	0.0000	0.0000	undef 0.0000
Sensory organs	0.0000	0.0000	undef 0.0000

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0056
Brain	0.0000
Brain	0.0039
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0000
Adrenal gland	0.0000
Kidney	0.0000
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Breast_t	0.0000
Large intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0058
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0097
Testicles_n	0.0000
Testicles_t	0.0000
Lungs_n	0.0098
Lungs_t	0.0000
Nerves	0.0040
Kidney_t	0.0000
Ovary uterus	0.0180
Prostate_n	0.0485
Sensory organs	0.0000
White blood cells	0.0000

Electronic Northern for Seq. ID: 241

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma	0.0000	0.0000	undef undef
Bladder	0.0000	0.0000	undef undef
Breast	0.0070	0.0098	0.7157 1.3973
Large intestine	0.0000	0.0000	undef undef
Small intestine	0.0000	0.0320	0.0000 undef
Ovary	0.0030	0.0024	1.2443 0.8036
Endocrine tissue	0.0032	0.0000	undef 0.0000
Brain	0.0012	0.0199	0.0580 17.2337
Skin	0.0000	0.0000	undef undef
Hepatic	0.0000	0.0000	undef undef
Heart	0.0061	0.0000	undef 0.0000
Testicles	0.0080	0.0000	undef 0.0000
Lung	0.0000	0.0000	undef undef
Stomach-esophagus	0.0000	0.0064	0.0000 undef
Muscle-skeleton	0.0000	0.0000	undef undef
Kidney	0.0045	0.0000	undef 0.0000
Pancreas	0.0000	0.0000	undef undef
Prostate	0.0085	0.0052	1.6279 0.6143
T lymphoma	0.0000	0.0000	undef undef
Uterus	0.0103	0.0000	undef 0.0000
White blood cells	0.0000	0.0000	undef undef
Hematopoietic	0.0107		
Penis	0.0000		
Seminal vesicle	0.0000		
Sensory organs	0.0000		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0028
Brain	0.0000
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0036
Lung	0.0036
Adrenal gland	0.0000
Kidney	0.0000
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0136
Breast_t	0.0000
Large intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0152
Endocrine tissue	0.0000
Fetal	0.0029
Gastrointestinal	0.0122
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles_n	0.0000
Testicles_t	0.0000
Lungs_n	0.0000
Lungs_t	0.0000
Nerves	0.0000
Kidney_t	0.0040
Ovary Uterus	0.0000
Prostate_n	0.0180
Sensory organs	0.0000
White blood cells	0.0000

Electronic Northern for Seq. ID: 242

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma	0.0000	0.0000	undef undef
Bladder	0.0000	0.0047	0.0000 undef
Breast	0.0018	0.0028	0.6262 1.5969
Large intestine	0.0057	0.0028	2.0184 0.4955
Small intestine	0.0000	0.0000	undef undef
Ovary	0.0030	0.0000	undef 0.0000
Endocrine tissue	0.0030	0.0035	1.3580 0.7364
Brain	0.0000	0.0000	undef undef
Skin	0.0000	0.0000	undef undef
Hepatic	0.0000	0.0000	undef undef
Heart	0.0030	0.0000	undef 0.0000
Testicles	0.0000	0.0000	undef undef
Lung	0.0000	0.0000	undef undef
Stomach-esophagus	0.0000	0.0000	undef undef
Muscle-skeleton	0.0000	0.0128	0.0000 undef
Kidney	0.0034	0.0000	undef 0.0000
Pancreas	0.0000	0.0000	undef undef
Prostate	0.0000	0.0000	undef undef
T lymphoma	0.0057	0.0026	2.1706 0.4607
Uterus	0.0000	0.0000	undef undef
White blood cells	0.0030	0.0046	0.6426 1.5563
Hematopoietic	0.0000	0.0000	undef undef
Penis	0.0000		
Seminal vesicle	0.0000		
Sensory organs	0.0000		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0036
Adrenal gland	0.0000
Kidney	0.0062
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0126

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Breast t	0.0000
Large Intestine_t	0.0000
Ovary n	0.0000
Ovary t	0.0000
Endocrine tissue	0.0000
Fetal	0.0000
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0032
Testicles n	0.0000
Testicles t	0.0000
Lungs n	0.0000
Lungs t	0.0000
Nerves	0.0030
Kidney t	0.0000
Ovary Uterus	0.0045
Prostate n	0.0121
Sensory organs	0.0000
White blood cells	0.0000

Electronic Northern for Seq. ID: 243

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
B lymphoma	0.0000	0.0000	undef	undef
Bladder	0.0000	0.0000	undef	undef
Breast	0.0026	0.0014	1.8786	0.5323
Large intestine	0.0038	0.0000	undef	0.0000
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0059	0.0000	undef	0.0000
Endocrine tissue	0.0032	0.0071	0.4527	2.2091
Brain	0.0012	0.0090	0.1289	7.7552
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0029	0.0018	1.5786	0.6335
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0017	0.0000	undef	0.0000
Pancreas	0.0022	0.0000	undef	0.0000
Prostate	0.0000	0.0000	undef	undef
T lymphoma	0.0047	0.0013	3.6176	0.2764
Uterus	0.0025	0.0000	undef	0.0000
White blood cells	0.0030	0.0092	0.3213	3.1125
Hematopoietic	0.0021	0.0000	undef	0.0000
Penis	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0125
Hematopoietic	0.0039
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0072
Adrenal gland	0.0000
Kidney	0.0000
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0251

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Breast_t	0.0000
Large intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0041
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0032
Testicles_n	0.0084
Testicles_t	0.0000
Lungs_n	0.0000
Lungs_t	0.0000
Nerves	0.0020
Kidney_t	0.0000
Ovary uterus	0.0180
Prostate_n	0.0121
Sensory organs	0.0000
White blood cells	0.0000

Electronic Northern for Seq. ID: 244

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma	0.0025	0.0000	undef 0.0000
Bladder	0.0117	0.0117	0.9957 1.0043
Breast	0.0097	0.0070	1.3777 0.7259
Large intestine	0.0077	0.0000	undef 0.0000
Small intestine	0.0165	0.0000	undef 0.0000
Ovary	0.0000	0.0048	0.0000 undef
Endocrine tissue	0.0080	0.0071	1.1317 0.8836
Brain	0.0075	0.0080	0.9429 1.0605
Skin	0.0000	0.0000	undef undef
Hepatic	0.0046	0.0063	0.7324 1.3653
Heart	0.0071	0.0000	undef 0.0000
Testicles	0.0120	0.0059	2.0357 0.4912
Lung	0.0049	0.0000	undef 0.0000
Stomach-esophagus	0.0072	0.0000	undef 0.0000
Muscle-skeleton	0.0171	0.0111	1.5463 0.6467
Kidney	0.0000	0.0000	undef undef
Pancreas	0.0050	0.0166	0.2992 3.3427
Prostate	0.0198	0.0078	2.5323 0.3949
T lymphoma	0.0051	0.0149	0.3381 2.9576
Uterus	0.0163	0.0046	3.5341 0.2930
White blood cells	0.0123	0.0000	undef 0.0000
Hematopoietic	0.0053		
Penis	0.0054		
Seminal vesicle	0.0141		
Sensory organs	0.0000		

FETUS
% freq.

Development	0.0139
Gastrointestinal	0.0111
Brain	0.0000
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0107
Lung	0.0145
Adrenal gland	0.0000
Kidney	0.0062
Placenta	0.0061
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0272
Breast t	0.0000
Large intestine_t	0.0000
Ovary n	0.0000
Ovary t	0.0000
Endocrine tissue	0.0245
Fetal	0.0081
Gastrointestinal	0.0244
Hematopoietic	0.0000
Skin-muscle	0.0259
Testicles n	0.0084
Testicles_t	0.0000
Lungs n	0.0000
Lungs_t	0.0000
Nerves	0.0000
Kidney t	0.0020
Ovary Uterus	0.0000
Prostate n	0.0090
Sensory organs	0.0000
White blood cells	0.0000

Electronic Northern for Seq. ID: 245

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma	0.0000	0.0000	undef undef
Bladder	0.0117	0.0117	0.9957 1.0043
Breast	0.0132	0.0084	1.5655 0.6388
Large intestine	0.0134	0.0028	4.7095 0.2123
Small intestine	0.0027	0.0107	0.2577 3.8812
Ovary	0.0030	0.0072	0.4148 2.4109
Endocrine tissue	0.0032	0.0106	0.3018 3.3136
Brain	0.0156	0.0070	2.2381 0.4468
Skin	0.0000	0.0000	undef undef
Hepatic	0.0093	0.0000	undef 0.0000
Heart	0.0122	0.0000	undef 0.0000
Testicles	0.0080	0.0000	undef 0.0000
Lung	0.0117	0.0037	3.1573 0.3167
Stomach-esophagus	0.0145	0.0000	undef 0.0000
Muscle-skeleton	0.0120	0.0000	undef 0.0000
Kidney	0.0045	0.0048	0.9285 1.0770
Pancreas	0.0033	0.0110	0.2992 3.3427
Prostate	0.0207	0.0000	undef 0.0000
T lymphoma	0.0025	0.0075	0.3381 2.9576
Uterus	0.0089	0.0138	0.6426 1.5563
White blood cells	0.0055	0.0607	0.0902 11.0896
Hematopoietic	0.0000		
Penis	0.0134		
Seminal vesicle	0.0000		
Sensory organs	0.0235		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0111
Brain	0.0000
Hematopoietic	0.0039
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0142
Lung	0.0145
Adrenal gland	0.0000
Kidney	0.0000
Placenta	0.0061
Prostate	0.0000
Sensory organs	0.0126

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0136
Breast_t	0.0000
Large intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0101
Endocrine tissue	0.0000
Fetal	0.0098
Gastrointestinal	0.0122
Hematopoietic	0.0000
Skin-muscle	0.0032
Testicles_n	0.0084
Testicles_t	0.0000
Lungs_n	0.0098
Lungs_t	0.0000
Nerves	0.0080
Kidney_t	0.0000
Ovary uterus	0.0135
Prostate_n	0.0061
Sensory organs	0.0387
White blood cells	0.0000

Electronic Northern for Seq. ID: 246

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma	0.0000	0.0000	undef undef
Bladder	0.0000	0.0141	0.0000 undef
Breast	0.0000	0.0042	0.0000 undef
Large intestine	0.0115	0.0028	4.0367 0.2477
Small intestine	0.0082	0.0000	undef 0.0000
Ovary	0.0000	0.0024	0.0000 undef
Endocrine tissue	0.0048	0.0053	0.9054 1.1045
Brain	0.0064	0.0030	2.1276 0.4700
Skin	0.0000	0.0000	undef undef
Hepatic	0.0046	0.0000	undef 0.0000
Heart	0.0051	0.0000	undef 0.0000
Testicles	0.0161	0.0059	2.7142 0.3684
Lung	0.0058	0.0074	0.7893 1.2669
Stomach-esophagus	0.0000	0.0000	undef undef
Muscle-skeleton	0.0051	0.0037	1.3917 0.7186
Kidney	0.0000	0.0000	undef undef
Pancreas	0.0017	0.0055	0.2992 3.3427
Prostate	0.0057	0.0026	2.1706 0.4607
T lymphoma	0.0000	0.0000	undef undef
Uterus	0.0044	0.0000	undef 0.0000
White blood cells	0.0014	0.0000	undef 0.0000
Hematopoietic	0.0000	0.0107	0.0000
Penis	0.0000	0.0000	0.0000
Seminal vesicle	0.0000	0.0000	0.0000
Sensory organs	0.0000	0.0000	0.0000

	FETUS % freq.
Development	0.0000
Gastrointestinal	0.0028
Brain	0.0188
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0036
Lung	0.0036
Adrenal gland	0.0000
Kidney	0.0000
Placenta	0.0061
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0136
Breast_t	0.0000
Large Intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0000
Gastrointestinal	0.0122
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles_n	0.0000
Testicles_t	0.0000
Lungs_n	0.0000
Lungs_t	0.0195
Nerve_s	0.0000
Kidney_t	0.0050
Ovary Uterus	0.0000
Prostate_n	0.0068
Sensory organs	0.0182
White blood cells	0.0000
	0.0000

Electronic Northern for Seq. ID: 247

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma	0.0025	0.0136	0.1840 5.4361
Bladder	0.0039	0.0023	1.6595 0.6026
Breast	0.0106	0.0056	1.8786 0.5323
Large intestine	0.0096	0.0142	0.6728 1.4864
Small intestine	0.0027	0.0000	undef 0.0000
Ovary	0.0030	0.0048	0.6222 1.6073
Endocrine tissue	0.0016	0.0231	0.0696 14.3590
Brain	0.0139	0.0040	3.4816 0.2872
Skin	0.0000	0.0000	undef undef
Hepatic	0.0093	0.0127	0.7324 1.3653
Heart	0.0081	0.0275	0.2954 3.3858
Testicles	0.0000	0.0118	0.0000 undef
Lung	0.0078	0.0092	0.8419 1.1877
Stomach-esophagus	0.0072	0.0128	0.5668 1.7644
Muscle-skeleton	0.0034	0.0000	undef 0.0000
Kidney	0.0112	0.0145	0.7737 1.2924
Pancreas	0.0066	0.0000	undef 0.0000
Prostate	0.0113	0.0065	1.7364 0.5759
T lymphoma	0.0152	0.0224	0.6762 1.4788
Uterus	0.0059	0.0000	undef 0.0000
White blood cells	0.0096	0.0607	0.1578 6.3369
Hematopoietic	0.0094		
Penis	0.0054		
Seminal vesicle	0.0000		
Sensory organs	0.0000		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0028
Brain	0.0000
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0260
Heart-blood vessels	0.0071
Lung	0.0036
Adrenal gland	0.0254
Kidney	0.0371
Placenta	0.0061
Prostate	0.0249
Sensory organs	0.0126

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0068
Breast_t	0.0000
Large intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0101
Endocrine tissue	0.0000
Fetal	0.0156
Gastrointestinal	0.0244
Hematopoietic	0.0000
Skin-muscle	0.0194
Testicles_n	0.0042
Testicles_t	0.0000
Lungs_n	0.0195
Lungs_t	0.0000
Nerves	0.0181
Kidney_t	0.0000
Ovary uterus	0.0180
Prostate_n	0.0121
Sensory organs	0.0232
White blood cells	0.0000

2.2. Fisher Test

In order to decide whether a partial sequence S of a gene occurs significantly more often or less often in a library for normal tissue than in a library for degenerated tissue, Fisher's exact test, a standard statistical process, is carried out (Hays, W. L., (1991) Statistics, Harcourt Brace College Publishers, Fort Worth).

The null hypothesis reads: The two libraries cannot be distinguished with respect to the frequency of sequences homologous to S. If the null hypothesis can be rejected with high enough certainty, the gene belonging to S is accepted as an advantageous candidate for a cancer gene, and in the next step an attempt is made to achieve lengthening of its sequence.

Example 3

Automatic lengthening of the partial sequence

Automatic lengthening of partial sequence S is completed in three steps:

1. Determination of all sequences homologous to S from the total set of available sequences using BLAST.
2. Assembling these sequences by means of the standard program GAP4 (Bonfield, J. K.; Smith, K.F. and Staden, R. (1995), Nucleic Acids Research 23 4992-4999) (contig formation).
3. Computation of a consensus sequence C from the assembled sequences.

The consensus sequence C will generally be longer than initial sequence S. Its electronic Northern Blot will

accordingly deviate from that for S. A repeated Fisher test decides whether the alternative hypothesis of deviation from a uniform expression in the two libraries can be maintained. If this is the case, an attempt is made to lengthen C in the same way as S. This iteration is continued with consensus sequences C_i (i: iteration index) obtained each time until the alternative hypothesis is rejected (if H_0 Exit; truncation criterion I) or until automatic lengthening is no longer possible (while $C_i > C_{i-1}$; truncation criterion II).

In the case of truncation criterion II, with the consensus sequence present after the last iteration, a complete or roughly complete sequence of a gene which can be related to cancer with high statistical certainty is acquired.

Analogously to the above described examples, it was possible to find the nucleic acid sequences described in Table I from prostate tumor tissue.

Furthermore, for the individual nucleic acid sequences, it was possible to determine the peptide sequences (ORFs) that are listed in Table II, in which no peptide can be assigned to a few nucleic acid sequences and more than one peptide can be assigned to some nucleic acid sequences. As already mentioned above, both the determined nucleic acid sequences and the peptide sequences assigned to the nucleic acid sequences are the subject of this invention.

Example 4**Mapping of nucleic acid sequences on the human genome**

Human genes were mapped using the Stanford G3 Hybrid Panel (Stewart et al., 1997), which is marketed by Research Genetics, Huntsville, Alabama. This panel consists of 83 different genomic DNAs of human-hamster hybrid cell lines and allows resolution of 500 kilobases. The hybrid cell lines were obtained by fusion of irradiated diploid human cells with cells of the Chinese hamster. The retention pattern of the human chromosome fragments is determined by means of gene-specific primers in a polymerase chain reaction and is analyzed using software available from the Stanford RH server (http://www.stanford.edu/RH/rhserver_form2.html). This program determines the STS marker which is nearest to the desired gene. The corresponding cytogenetic band was determined using the "Mapview" program of the Genome Database (GDB), (<http://gdbwww.dkfz-heidelberg.de>).

In addition to mapping of genes on the human chromosome set by various experimental methods, it is possible to determine the location of genes on this by biocomputer methods. To do this, the known program e-PCR was used (Schuler GD (1998) Electronic PCR: Bridging the gap between genome mapping and genome sequencing. Trends Biotechnol 16: 456-459, Schuler GD (1997). Sequence mapping by electronic PCR. Genome Res. 7; 541-550). The database used here no longer corresponds to the one cited in the literature, but is a development which includes data from the public database RHdb (<http://www.ebi.ac.uk/RHdb/index.html>). Analogously to the mapping by the hybrid panels, the results were

evaluated with the aforementioned software and the software of the Whitehead Institute (<http://carbon.wi.mit.edu:8000/cgi-bin/contig/rhmapper.pl>).

Example 5

Obtaining genomic DNA sequences (BAC clones)

The genomic BAC clones containing the corresponding cDNAs (<http://www.tree.caltech.edu/>; Shizuya, H.; B. Birren, U-J. Kim, V. Mancino, T. Slepak, Y. Tachiiri, M. Simon (1992) Proc. Natl. Acad. Sci., USA 89: 8794-8797) were isolated with the procedure of "down-to-the-well". In this procedure, a library consisting of BAC clones (the library covers roughly 3x the human genome) is moved into a certain raster, so that the DNA of these clones with a specific PCR can be studied. In doing so, "pooling" of the DNA of different BAC clones takes place. Combinatorial analysis makes it possible to determine the clones that contain the desired DNA. By fixing the clones, the address of the clones in the library can be determined. This address together with the name of the library which is being used unequivocally fixes the clones and thus the DNA sequence of these clones.

The following examples explain the successful isolation of the genomic BAC clones without limiting them thereto.

The libraries used were CITB B and CITB C:

Seq.ID No.	Identified BACs		
3	320-L-23		
4	461-O-11		
8	283-P-15	322-B-7	317-H-19
24	272-N-9	340-L-19	554-D-3
31	293-K-21	337-I-17	363-J-15
46	410-A-9		
47	268-B-2	532-B-10	

Table 1

Col. 1 - Seq ID
 Col. 2 - Expression
 Col. 3 - Function
 Col. 4 - Modules
 Col. 5 - Cytogenetic localization
 Col. 6 - Nearest marker
 Col. 7 - Length of initial EST in bases
 Col. 8 - Length of claimed sequence in bases
 Col. 9 - Seq ID of initial sequence

Table 1

Seq ID	Expression	Funktion	Module	Cytogenetische Lokalisation	Nächster Marker	Länge des Ausgangs-EST in Basen	Länge der beanspruchten Sequenz in Basen	Seq ID der Ausgangssequenz
2	im normalen Prostata- und Brustgewebe erhöht	ZYXIN 2	LIM	7q33-7q35	D7S661	202	1437	
3	in gesundem Prostata- und Brustgewebe erhöht	Unbekannt		17p13.3	D17S2199-D17S1548	207	707	
4	im normalen Prostata- und Brustgewebe erhöht	PCCMT		1p36.31	D1S2145-D1S2132	215	1265	
6	im normalen Prostata- und Brustgewebe erhöht	Unbekannt	UBIQUITIN_CONJUGAT_2	1q21.2	D1S3384-D1S305	225	1330	
7	im normalen Prostata- und Brustgewebe erhöht	Unbekannt		11q11-q13.1	D11S4205-D11S4535	231	762	
8	im normalen Prostata- und Brustgewebe erhöht	Humanes Homolog des TEGT-Proteins aus der Ratte		10q23.1	D10S551-D10S532	246	1228	
9	im normalen Blasen- und Prostata- und Brustgewebe erhöht	SRP20	rrm	6p21.2	NIB1566-WI-4186	243	914	
10	4x stärker als im normalen Prostata- und Brustgewebe	Muf1		1p33-p32.3	D1S1558-D1S232	315	1126	
12	im normalen Prostata- und Brustgewebe erhöht	Unbekannt		7p21.3-7p14.1	D7S2363	219	538	
13	im normalen Prostata- und Brustgewebe erhöht	Unbekannt		22q12.1 - 22q13.1	D22S1144	210	321	
14	ausschließlich in der normalen Prostata	E4BP4	B_ZIP	9q22.1-q22.2	D9S767	217	847	
16	stärker im normalen Brust- und Prostata- und Brustgewebe als im entsprechenden Tumor	HUMANER PHOSPHOLEMMAN PRECURSOR		19q13.1		210	573	
17	verstärkt in der normalen Prostata, verglichen mit dem entsprechenden Tumorgewebe	Mögliches Humans Homolog zu S1R		12q13.13 - 12q14.1	D12S1700-D12S1601	244	486	

Table 1

Seq ID	Expression	Function
2	elevated in normal prostate tissue	ZYXIN 2
3	elevated in healthy prostate and breast tissue	Unknown
4	elevated in normal prostate tissue	PCCMT
6	elevated in normal prostate tissue	Unknown
7	elevated in normal prostate tissue	Unknown
8	elevated in normal prostate tissue	Human homolog of TEGT protein from rats
9	elevated in normal bladder and prostate tissue	SRP20
10	4x more heavily than in normal prostate tissue	Muf1
12	elevated in normal prostate tissue	Unknown
13	elevated in normal prostate tissue	Unknown
14	solely in normal prostate	E4BP4
16	more heavily in normal breast and prostate tissue than in the corresponding tumor	HUMAN PHOSPHOLEMMAN PRECURSOR
17	intensified in normal prostate, compared to corresponding tumor tissue	Possible human homolog to S1R

UBIQUITIN_CONJUGAT_2 = UBIQUITIN_CONJUGATE_2

Seq ID	Expression	Function
18	about 6x more heavily in normal prostate compared to corresponding tumor tissue	Unknown
19	about 2x more heavily in normal prostate tissue than in corresponding tumor tissue	Unknown
21	about 3x more heavily in normal prostate tissue than in corresponding tumor tissue, about 7x more often in breast and lung tumors than in corresponding normal tissue	Homolog to JANUS-A from <i>Drosophila melanogaster</i>
23	more heavily in normal prostate tissue than in corresponding tumor tissue	Unknown
24	5x more heavily in normal prostate tissue than in corresponding tumor tissue, strongly expressed in skin tumors	ElF-6

Seq ID	Expression	Funktion	Module	Cytogenetische Lokalisation	Nächster Marker	Länge des Ausgangs-EST in Basen	Länge der beanspruchten Sequenz in Basen	Seq ID der Ausgangssequenz
18	ca. 6x stärker in der normalen Prostata, verglichen mit dem entsprechenden Tumorgewebe	Unbekannt		10q23.32 - 10q24.31	D10S551-D10S532	215	662	
19	ca. 2x stärker im normalen Prostata-gewebe als im entsprechenden Tumorgewebe	Unbekannt		2q35	D2S433-D2S295	225	750	
21	ca. 3x stärker im normalen Prostata-gewebe als im entsprechenden Tumorgewebe, ca. 7x häufiger in Brust- und Lungentumoren als in entsprechenden Normalgeweben	Homolog zu JANUS-A aus <i>Drosophila melanogaster</i>		9q34.13	D9S158-D9S2053	229	1001	
23	stärker im normalen Prostata-gewebe als im entsprechenden Tumorgewebe	Unbekannt		1p36.13-p32.3	SGC32968	184	580	
24	5x stärker im normalen Prostata-gewebe als im entsprechenden Tumorgewebe, stark exprimiert in Hauttumoren	ElF-6		20q11.1-q11.22		237	740	

Seq ID	Expression	Function
26	more heavily in normal prostate tissue than in corresponding tumor tissue	Homolog to HUMAN SORCIN
27	more heavily in normal prostate tissue than in corresponding tumor tissue	Unknown
28	about 3x more heavily in normal prostate tissue than in corresponding tumor tissue	Unknown
29	more heavily in normal prostate tissue than in corresponding tumor tissue	IL-6SAG
30	about 4x more heavily in normal prostate tissue than in corresponding tumor tissue	Unknown
31	more heavily in normal prostate tissue than in corresponding tumor tissue	Unknown
32	more heavily in normal prostate tissue than in corresponding tumor tissue, elevated 10x in muscle and skeletal tumors	Unknown

Seq ID	Expression	Funktion	Module	Cytogenetische Lokalisation	Nächster Marker	Longe des Ausgangs-EST in Basen	Longe der beanspruchten Sequenz in Basen	Seq ID der Ausgangssequenz
26	stärker im normalen Prostatagewebe als im entsprechenden Tumorgewebe	Homolog zu HUMANem SORCIN		1p36 11-p34 3	D1S233-D1S2548	219	975	
27	stärker im normalen Prostatagewebe als im entsprechenden Tumorgewebe	Unbekannt		9p21 1-q12	SHGC-7278-SHGC-33912	259	854	
28	ca. 3x stärker im normalen Prostatagewebe als im entsprechenden Tumorgewebe	Unbekannt		11q12 1-11q13 5	SHGC-15247-NIB715	288	802	
29	stärker im normalen Prostatagewebe als im entsprechenden Tumorgewebe	IL-6SAG		20p11 23-p11 21	D20S807-SHGC-11944	224	807	
30	ca. 4x stärker im normalen Prostatagewebe als im entsprechenden Tumorgewebe	Unbekannt		Xp11 23-p11 21	WI-5587-WI-5717	276	777	
31	stärker im normalen Prostatagewebe als im entsprechenden Tumorgewebe	Unbekannt				238	501	
32	stärker im normalen Prostatagewebe als im entsprechenden Tumorgewebe, 10x erhöht in Muskel- und Skelettumoren	Unbekannt		3p21 1 - 3p22 2	WI-9590-WI-3521	284	1104	

Seq. ID	Expression	Function
33	elevated in normal prostate tissue	Human homolog of WW-domain binding protein 1 from mice
35	elevated in normal prostate tissue and in gastrointestinal tumors	Unknown
36	elevated in normal prostate tissue	Id1
37	elevated in normal prostate tissue	Unknown
39	elevated in prostate tumors	C1 inhibitor
41	more heavily in normal prostate tissue than in corresponding tumor tissue	Acyl-protein thioesterase
42	more heavily in normal prostate tissue than in corresponding tumor tissue	Unknown
43	about 6x more heavily in normal prostate tissue than in corresponding tumor tissue	Unknown

Seq ID	Expression	Funktion	Module	Cytogenetische Lokalisation	Nächster Marker	Länge des Ausgangs-EST in Basen	Länge der beanspruchten Sequenz in Basen	Seq ID der Ausgangssequenz
33	in normalem Prostatagewebe erhöht	Humanes Homolog des WW-domain binding protein 1 aus der Maus		2p13.1	D2S145-SHGC-37085	208		810
35	in normalem Prostatagewebe und in gastrointestinalen Tumoren erhöht	Unbekannt		3p23-p21.1	SHGC-32684-D3S4190	223		826
36	in normalem Prostatagewebe erhöht	Id1	HLH	20p11.22 - 20q11.21	Wt-1163	254		578
37	in normalem Prostatagewebe erhöht	Unbekannt		8p12	SHGC-5722-SHGC-5765	293		799
39	in Prostata Tumoren erhöht	C1 inhibitor	serpin	11p13-11q13.1	SHGC-30227-D11S1983	262		1743
41	stärker in normalem Prostatagewebe als im entsprechenden Tumorgewebe	Acyl-protein thioesterase		6p21.31-q21.2	D6S1988-D6S1987	267		1183
42	stärker in normalem Prostatagewebe als im entsprechenden Tumorgewebe	Unbekannt		16q12.1-22.1	SHGC-6119-SHGC-15371	270		768
43	ca. 6x stärker in normalem Prostatagewebe als im entsprechenden Tumorgewebe	Unbekannt		17q11.2-q21.31	SHGC-30259-SHGC-13493	279		1029

Seq. ID	Expression	Function
44	about 3x more heavily in normal prostate tissue than in corresponding tumor tissue, about 8x more often in a brain tumor than in comparable normal tissue	Unknown
46	elevated in normal prostate tissue	Unknown
47	elevated in normal prostatic, hepatic and ovarian tissue	Unknown
51	elevated in normal prostate tissue and hematopoietic tumors	Unknown
52	elevated in normal prostate tissue and in brain tumors	SPARC
53	elevated in normal prostate tissue	Unknown
51	elevated in normal prostate tissue and in skeletal tumors	Unknown
55	elevated in normal prostate tissue and hepatic tumors	B4-2

Seq ID	Expression	Funktion	Module	Cytogenetische Lokalisation	Nächster Marker	Länge des Ausgangs-EST in Basen	Länge der beanspruchten Sequenz in Basen	Seq ID der Ausgangssequenz
44	ca. 3x stärker in normalem Prostata-gewebe als im entsprechenden Tumorgewebe, ca. 8x häufiger im Gehirntumor als im vergleichbaren Normalgewebe	Unbekannt		16q23 1-q24 2	SHGC-32665-SHGC-11833	237	736	
46	in normalem Prostata-gewebe erhöht	Unbekannt		19p13 3	IB1264-WI-6480	259	1159	
47	in normalem prostaticen, hepatischen und ovarial Gewebe erhöht	Unbekannt		6q13-q21		159	690	
51	in normalem Prostata-gewebe und in hämatopoetischen Tumoren erhöht	Unbekannt		1p36 11	D1S3131-D1S2674	250	1188	
52	in normalem Prostata-gewebe und in Gehirntumoren erhöht	SPARC	kazal	5q21 1-q33.2	WI-7565-WI-6351	261	1029	
53	in normalem Prostata-gewebe erhöht	Unbekannt		15q23-24.1	D1S1241-D1S197	261	985	
54	in normalem Prostata-gewebe und in Skelettumoren erhöht	Unbekannt		4p14	D4S406-SHGC-9448	246	622	
55	in normalem Prostata-gewebe und hepatischen Tumoren erhöht	B4-2		6q16 2	D6S1644-D6S2057	239	1129	

Seq. ID	Expression	Function
58	about 3x more heavily in normal prostate tissue than in corresponding tumor tissue	Unknown
59	about 5x more heavily in normal prostate tissue than in corresponding tumor tissue	Methyl-CpG binding protein MBD2
60	more heavily in normal prostate tissue than in corresponding tumor tissue	Unknown
61	elevated in normal prostate tissue and in endocrine tumors	Unknown
62	elevated in normal prostate and breast tissue	Unknown
63	elevated in normal prostate, bladder and breast tumors	Unknown
64	expressed 1.8088x in benign prostate tissue	Homolog to RanBP7
217	expressed 2.894x in benign prostate tissue compared to the prostate tumor	Unknown

Seq ID	Expression	Funktion	Module	Cytogenetische Lokalisation	Nächster Marker	Länge des Ausgangs-EST in Basen	Länge der beanspruchten Sequenz in Basen	Seq ID der Ausgangssequenz
58	ca. 3x stärker in normalem Prostatagewebe als in entsprechenden Tumorgewebe	Unbekannt		1q12	SHGC-32015-D1S442	160	877	
59	ca. 5x stärker in normalem Prostatagewebe als in entsprechenden Tumorgewebe	Methyl-CpG bindendes Protein MBD2		18q21.32-18q21.32		288	1329	
60	stärker in normalem Prostatagewebe als in entsprechenden Tumorgewebe	Unbekannt		11q21-11q23.2		310	697	
61	in normalem Prostatagewebe und in endokrinen Tumoren erhöht	Unbekannt		17p11.2	AFMA126YD5	378	1389	
62	in normalem Prostata- und Brustgewebe erhöht	Unbekannt		4q21.21-4q21.23	WI-7565-WI-9200	260	535	
63	in normalem Prostata-, Blasen- und Brusttumoren erhöht	Unbekannt		16p12.3-16p13.11	AFMB354YF9	216	1098	
64	1.8088 x im gutartigen Prostatagewebe exprimiert	Homolog zu RanBP7		11p15.3-p15.5	D11S909-D11S4149	302	1860	
217	2.894 x im gutartigen Prostatagewebe gegenüber dem Prostata-tumor exprimiert	Unbekannt	UBIQUITIN_CONJUGAT	1q21.2	D1S3384-D1S305		1860	6

Seq ID	Expression	Function
218	expressed 2.1705x in benign prostate tissue compared to the prostate tumor	Unknown
219	expressed 2.7494x in benign prostate tissue compared to the prostate tumor	Human homolog of TEGT from rats
221	expressed 2.46x in benign prostate tissue compared to the prostate tumor	TXBP151
221	expressed 1.7364x in benign prostate tissue compared to the prostate tumor	Possible human homolog to S1R
222	expressed 2.8941x in benign prostate tissue compared to the prostate tumor	Unknown
223	expressed 0.8348x in benign prostate tissue compared to the prostate tumor	Homolog to HYA22
224	expressed 1.0129x in benign prostate tissue compared to the prostate tumor	Unknown

Seq ID	Expression	Funktion	Module	Cytogenetische Lokalisation	Nachster Marker	Länge des Ausgangs-EST in Basen	Länge der beanspruchten Sequenz in Basen	Seq ID der Ausgangssequenz
218	2.1705 x im gutartigen Prostatagewebe gegenüber dem Prostataumor exprimiert	Unbekannt		11q11-q13.1	D11S4205-D11S4535		1024	7
219	2.7494 x im gutartigen Prostatagewebe gegenüber dem Prostataumor exprimiert	Humanes Homolog des TEGT aus der Ratte		10q23.1	D10S551-D10S532		2383	8
220	2.46 x im gutartigen Prostatagewebe gegenüber dem Prostataumor exprimiert	TXBP151	COILS	7p21.3-7p14.1	D7S2363		3210	12
221	1.7364 x im gutartigen Prostatagewebe gegenüber dem Prostataumor exprimiert	Mögliches Humans Homolog zu S1R		12q13.13-12q14.1	D12S1700-D12S1601		1030	17
222	2.8941 x im gutartigen Prostatagewebe gegenüber dem Prostataumor exprimiert	Unbekannt		10q23.32-10q24.31	D10S551-D10S532		1216	16
223	0.8348 x im gutartigen Prostatagewebe gegenüber dem Prostataumor exprimiert	Homolog zu HYA22		2q35	D2S433-D2S295		2369	19
224	1.0129 x im gutartigen Prostatagewebe gegenüber dem Prostataumor exprimiert	Unbekannt		1p36.13-p32.3	SGC32966		849	23

Seq. ID	Expression	Function
225	expressed 8.6822x in benign prostate tissue compared to the prostate tumor	Homolog to HUMAN SORCIN
226	No similar sequence was found in the prostate tumor	Unknown
227	expressed 2.4117x in benign prostate tissue compared to the prostate tumor	IL-6SAG
228	expressed 2.1706x in benign prostate tissue compared to the prostate tumor	Unknown
229	No similar sequence was found in the prostate tumor	Unknown
230	expressed 1.447x in benign prostate tissue compared to the prostate tumor	Unknown
231	expressed 2.6529x in benign prostate tissue compared to the prostate tumor	Human homolog of WW-domain binding protein 1 from mice
232	expressed 3.1353x in benign prostate tissue compared to the prostate tumor	Homolog to OLIGOSACCHARYL TRANSFERASE STT3 subunit from C. elegans

Seq ID	Expression	Funktion	Module	Cytogenetische Lokalisation	Nächster Marker	Länge des Ausgangs-EST in Basen	Länge der beanspruchten Sequenz in Basen	Seq ID der Ausgangssequenz
225	8.6822 x im gutartigen Prostatagewebe gegenüber dem Prostata-tumor exprimiert	Homolog zu HUMANem SORCIN	EF_HAND_2	1p36.11-p34.3	D1S233-D1S2548		1502	26
226	Es wurde keine ähnliche Sequenz im Prostata-tumor gefunden	Unbekannt		9p21.1-9q12	SHGC-7278-SHGC-33912		1892	27
227	2.4117 x im gutartigen Prostatagewebe gegenüber dem Prostata-tumor exprimiert	IL-6SAG		20p11.23-p11.21	D20S807-SHGC-11944		1522	29
228	2.1706 x im gutartigen Prostatagewebe gegenüber dem Prostata-tumor exprimiert	Unbekannt		Xp11.23-p11.21	WI-5587-WI-5717		2016	30
229	Es wurde keine ähnliche Sequenz im Prostata-tumor gefunden	Unbekannt					765	31
230	1.447 x im gutartigen Prostatagewebe gegenüber dem Prostata-tumor exprimiert	Unbekannt		3p21.1 - 3p22.2	WI-9590-WI-3521		1611	32
231	2.6529 x im gutartigen Prostatagewebe gegenüber dem Prostata-tumor exprimiert	Humanes Homolog des WW-domain binding protein 1 aus der Maus		2p13.1	D2S145-SHGC-37085		1473	33
232	3.1353 x im gutartigen Prostatagewebe gegenüber dem Prostata-tumor exprimiert	Homolog zu der OLIGOSACCHARYL TRANSFERASE STT3 Untereinheit aus C. elegans		3p23-p21.1	SHGC-32684-D3S4150		2503	35

Seq. ID	Expression	Function
233	expressed 2.7132x in benign prostate tissue compared to the prostate tumor	Unknown
234	No similar sequence was found in the prostate tumor	Acyl-protein thioesterase
235	No similar sequence was found in the prostate tumor	Unknown
236	expressed 2.6529x in benign prostate tissue compared to the prostate tumor	Stat5b
237	expressed 3.2558x in benign prostate tissue compared to the prostate tumor	Unknown
238	expressed 4.3411x in benign prostate tissue compared to the prostate tumor	Unknown
239	expressed 3.1353x in benign prostate tissue compared to the prostate tumor	SDP3
240	expressed 1.447x in benign prostate tissue compared to the prostate tumor	Unknown

Seq ID	Expression	Funktion	Module	Cytogenetische Lokalisation	Nächster Marker	Länge des Ausgangs-EST in Basen	Länge der beanspruchten Sequenz in Basen	Seq ID der Ausgangssequenz
233	2.7132 x im gutartigen Prostatagewebe gegenüber dem Prostata-tumor exprimiert	Unbekannt		8p12	SHGC-5722-SHGC-5765		1756	37
234	Es wurde kein ähnliche Sequenz im Prostata-tumor gefunden	Acyl-protein thioesterase		6p21 31-q21 2	D6S1868-D6S1867		1286	41
235	Es wurde kein ähnliche Sequenz im Prostata-tumor gefunden	Unbekannt		16q12 1-22 1	SHGC-6119-SHGC-15371		1230	42
236	2.6529 x im gutartigen Prostatagewebe gegenüber dem Prostata-tumor exprimiert	Stat5b		17q11 2-q21 31	SHGC-30259-SHGC-13493		2328	43
237	3.2558 x im gutartigen Prostatagewebe gegenüber dem Prostata-tumor exprimiert	Unbekannt		16q23 1-q24 2	SHGC-32665-SHGC-11833		1767	44
238	4.3411 x im gutartigen Prostatagewebe gegenüber dem Prostata-tumor exprimiert	Unbekannt		19p13 3	IB1264-WI-6480		2311	46
239	3.1353 x im gutartigen Prostatagewebe gegenüber dem Prostata-tumor exprimiert	SDP3	PX	6q13-q21			1772	47
240	1.447 x im gutartigen Prostatagewebe gegenüber dem Prostata-tumor exprimiert	Unbekannt		1p36 11	D1S3131-D1S2674		2409	51

Seq ID	Expression	Function
241	expressed 1.6279x in benign prostate tissue compared to the prostate tumor	Unknown
242	expressed 2.1706x in benign prostate tissue compared to the prostate tumor	Unknown
243	expressed 3.6176x in benign prostate tissue compared to the prostate tumor	Unknown
244	expressed 2.5323x in benign prostate tissue compared to the prostate tumor	Unknown
245	No similar sequence was found in the prostate tumor	LIMP II
246	expressed 2.1706x in benign prostate tissue compared to the prostate tumor	Unknown
247	expressed 1.7364x in benign prostate tissue compared to the prostate tumor	Homolog to RanBP7

Seq ID	Expression	Funktion	Module	Cytogenetische Lokalisation	Nächster Marker	Länge des Ausgangs-EST in Basen	Länge der beanspruchten Sequenz in Basen	Seq ID der Ausgangssequenz
241	1.6279 x im gutartigen Prostatagewebe gegenüber dem Prostata-tumor exprimiert	Unbekannt		15q23-24 1	D15S1241-D15S197		2594	53
242	2.1706 x im gutartigen Prostatagewebe gegenüber dem Prostata-tumor exprimiert	Unbekannt		4p14	D4S405-SHGC-9448		1012	54
243	3.6176 x im gutartigen Prostatagewebe gegenüber dem Prostata-tumor exprimiert	Unbekannt		1q12	SHGC-32015-D1S442		1208	58
244	2.5323 x im gutartigen Prostatagewebe gegenüber dem Prostata-tumor exprimiert	Unbekannt		17p11 2	AFMA126YD5		2514	61
245	Es wurde keine ähnliche Sequenz im Prostata-tumor gefunden	LIMP II	CD36	4q21.21 - 4q21 23	WI-7565-WI-9200		3903	62
246	2.1706 x im gutartigen Prostatagewebe gegenüber dem Prostata-tumor exprimiert	Unbekannt		16p12 3 - 16p13 11	AFM8354YF9		1730	63
247	1.7364 x im gutartigen Prostatagewebe gegenüber dem Prostata-tumor exprimiert	Homolog zu RanBP7		11p15 3-p15 5	D11S909-D11S4149		3439	64

Table 2

<u>DNA Sequence</u> <u>ID No.</u>	<u>ORF Sequence ID No.</u>			
2	66			
3	67	68	69	70
4	71			
6	73			
7	74			
8	75			
9	82			
10	83			
12	90			
14	91			
16	92			
17	93			
18	97	98	99	100 101
19	102	103	104	105
21	109			
23	111	112	113	
24	114			
26	116			
27	117	118	119	
28	120	121	122	123 124
29	128			
30	129	130	131	
31	132			
32	133			
33	134	135	136	137
35	139	140	141	142 143 144 145 146
36	147	148	149	
39	152			
41	154	155	156	157
42	158	159	160	161
43	162	163	164	
44	165			
46	168	169	170	171 172
47	173			
51	183	184	185	186 187
52	188	189	190	191 192 193
54	194			
55	195			
58	201			
59	202	203	204	205 206
60	207	208	209	
61	210			
62	214	215	216	
217	248			
218	249	250		
219	251			
220	252			
221	253			

<u>DNA Sequence</u>	<u>ORF Sequence</u>
<u>ID No.</u>	<u>ID No.</u>
222	254 255
223	256
224	257
225	258
226	259 260
227	261 262
228	263
229	264 265
230	266
231	267 268
232	269
233	270 271
234	272 273
235	274 275
236	276
237	277
238	280 281
239	282
240	283 284
241	285 286
242	287 288
243	289 290
244	291 292
245	293
246	294
247	295

The inventive nucleic acid sequences Seq. ID No. 2-4, 6-10, 12-14, 16-19, 21, 23, 24, 26-33, 35-37, 39, 41-44, 46, 47, 49, 51-55, 58-64 and Seq. ID No. 217-247 of the determined candidate genes and the determined amino acid sequences Seq. ID No. 66-71, 73-75, 82, 83, 90-93, 97-105, 109, 111-114, 116-124, 128-137, 139-149, 152, 154-165, 168-173, 183-195, 214-216 and up to Seq. ID No. 248-295 are described in the following sequence protocol.

Sequence protocol**(1) GENERAL INFORMATION:****(i) APPLICANT**

- (A) NAME: metaGen - Gesellschaft fuer Genomforschung mbH
- (B) STREET: Ihnestrassse 63
- (C) CITY: Berlin
- (E) COUNTRY: Germany
- (F) POSTAL CODE (ZIP) D-14195
- (G) TELEPHONE: (030)-8413 1672
- (H) FAX: (030)-8413 1671

(ii) TITLE OF INVENTION: Human Nucleic Acid Sequences from Prostate Tissue**(iii) Number of sequences: 216****(iv) COMPUTER READABLE FORM:**

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: Patentin release #1.0 version #1.25 (EPO)

(2) INFORMATION ON SEQ ID NO. 2:**(i) SEQUENCE CHARACTERISTIC:**

- (A) LENGTH: 1437 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing**(iii) HYPOTHETICAL: NO****(iii) ANTI-SENSE: NO****(vi) ORIGIN:**

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

```

CTCCTTGGA  GTCCCCCTCC AGCTCCAGC CTCTGCCCA GGTTCGGGT CCGGCTCAGA 60
GCCAGACACA GTTCCATGTT CAGCCCCAGC CCCAGCCCAA GCCTCAGGTC CAACTCCATG 120
TCCAGTCCCA GACCCAGCCT GTGTCTTTGG CTAACACCCA GCGCCGAGGG CCCCCAGCCT 180
CATCTCCGGC TCCAGCCCTT AAGTTTCTC CAGTGA CTCC TAAGTTTACT CCTGTGGCTT 240
CCAAGTTCAG TCCTGGAGCC CCAAGTGGAT CTGGGTCA CA ACCAAATCAA AAATTGGGGC 300
ACCCCGAAGC TCTTTCTGCT GGCACAGGCT CCCCTCAACC TCCAGCTTC ACCTATGCCC 360
AGCAGAGGGA GAAGCCCCGA GTGCAGGAGA AGCAGCACCC CGTGCCCCCA CCGGCTCAGA 420
ACCAAAACCA GGTGGGCTCC CCTGGGGCCC CAGGGCCCCC GACTCTGAAG GAGGTGGAG 480
AGCTGGAGCA GCTGACCCAG CAGCTAATGC AGGACATGGA GCATCCTCAG AGGCAGAATG 540
TGCTGTCAA CGAACTCTGC GGCCGATGCC ATCAACCCCT GGCCCGGGCG CAGCAGCCGT 600
CCGCGCTCTA GGGCAGCTGT TCCACATGCG CTGCTTACCC TGCCACCAGT GTCCGCAGAG 660
CTCCAGGGCC AGCAGTTCTA TCTGTGGAG GGGCGCGCGT ACTGCGAGGG CTGTTACACT 720
GACACCTGG AGAAGTGTAT TGGCGG GAGCCCATCA CTGACCGCAT GCTGAGGGGC 780
ACGGGCAAGG CCTATCACCC GACTGCTTC ACCTGTGTGG TCTGCGCCCG CCCCCTGGAG 840
GGCACCTCCT TCATCGTGA CAGGCCAAC CGGCCCACT GTGTCCCGGA CTACCAACA 900
CAGTACGCCC CGAGGTGCTC CGTCTGCTCT GAGCCCATCA TGCCGTGAGC TGGCCGAGAT 960
GAGACTGTGC GAGTGGTGGC CCTGGACAAG AACTTCCACA TGAAGTGTTA CAAGTGTGAG 1020
GACTGCGGGA AGCCCTGTG GATTGAGGCA GATGACAATG GCTGCTTCCC CTTGGACGGT 1080
CACGTGCTCT GTCCGAAGTG CCACACTGCT AGAGCCAGA CCTGAGTGAG GACAGGCCCT 1140
CTTCAGACCG CAGTCCATGC CCCATTGTGG ACCACCCACA CTGAGACCAC CTGCCCCAC 1200
CTCAGTTAT GTTTTGATGT CTAGCCCTC CCAATTCCAA CCCCTCCCTA GCATCCCAGG 1260
TGCCCTGACC CAGGACCCAA CATGGTCTAG GGATGCAGGA TCCCCGCCCT GGGGTCTGGT 1320
CCTCGCCCAT CCTGCAGGGA TTGCCACCG TCTTCAGAC ACCCCACCTG AGGGGGGCAC 1380
AAGGTTAGT GCTGCTGCTT TCATGCTGC ACCCGCGCCC TCGCCGGGCC CCCCAGAG 1437

```

(2) INFORMATION ON SEQ ID NO. 3:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 707 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

TGCGGCCCGG	GCCTTAAAGC	GTCCATTTC	CAGCGGCCCT	CCGCTGCGAG	ACCGCAGCCC	60
TTCTCTGGAG	TCTCAGAGCC	GCAAGACACC	ACGACTCCCA	GAGGACCTTG	CGTCGGGCAA	120
GAAAGACTAC	ACCTTCCAGA	GGCCTCTGCG	GCGCCGCGAC	AGGAAGCGGC	GGGCGAGCCG	180
AGTGTCTTIG	CGCGTGGATC	CGAGCGACCA	TGGTGGCCCG	GGTGTGGTGC	CTGATGAGGT	240
TCCTCATCAA	GGGAAGTGTG	GCTGGGGGCG	CCGTCTACCT	GGTGTACGAC	CAGGAGCTGC	300
TGGGGCCCCAG	CGACAAGAGC	CAGGCAGCCC	TACAGAAGGC	TGGGGAGGTG	GTCCCCCCCC	360
CCATGTACCA	GTTCAGCCAG	TACGTGTGTC	AGCAGACAGG	CCTGCAGATA	CCCCAGCTCC	420
CAGCCCCCTCC	AAAGATTAC	TTTCCCATCC	GTGACTCCTG	GAATGCAGGC	ATCATGACGG	480
TGATGTCAGC	TCTGTCGGTG	GCCCCCTCCA	AGGCCCGCGA	GTACTCCAAG	GAGGGGTGGG	540
AGTATGTGAA	GGCGCGCACC	AAGTAGCGAG	TCAGCAGGGC	CGCCTGCCCC	GGCAGAACC	600
GGCAGGGCTG	CCACTGACCT	GAAGACTCCG	GACTGGGACC	CCACTCCGAG	GGCAGGCCTC	660
CCGATTGCCG	GCCCAATAAA	GGACTTCAGA	AGTGAAAAAA	AAAAAAA		707

(2) INFORMATION ON SEQ ID NO. 4:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1265 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

```

CACTGGGATG GGCATACACT ACTCACAGGG TGTGTGAGAT GAGAAGAACA CGTCAANGTT 60
TTTATACTCA GATGTGGGAG CGACATCAAT GAAATCTGTA CTGTATGAAA GCTACACAAA 120
AATGGGCAGA CATTGGGTTA ATTGTGCCAG ATACCTAAAA TGTATGTTCA GAAAAGCATT 180
TTATCAACTC AGAAATATGA CTTATTCTTA GATTTCATGG CTTAATGAAT TTTTTCATTG 240
TTATATATAC CAAAGAGGCT TACGGGTTCA TTGATTGGTT TGAACCACAG ACAGACGGCC 300
GTGAGCCACC ACGCCAGGCC AAGATGAAC CTCTAAGGAC AGGATTGGT AAGTGATTGA 360
CTTCTTTTGA GTTCCATGAT CTTGAGATTA TTTTtagcTT TATAAATTTA GCAGTGGCAG 420
GGCCCGTGGG GAATCAGGTT AATGAGGTAA AGGCTTCTG GGTATTGGT GCCAAGGCCA 480
CATCACC AAT TTTCTCGATT TAAAAAAGT TCAAGAGATT TATTTTCCA TTGCAGGTTT 540
TAAAGTGGAG ATTCTGAAGT GGAAAATAGG TACTGTCAGA ACAAAGCTAC CTGGAACAG 600
CATAGACTGA AGCCTTTCGT GAGGGCTTGC AGGCCGCTGC TGAGTGGCAG TTTACAGAG 660
AGGTCGCGGG GTGAGCCTCT TAGCAGGACA GAAAACAAGG CAGCAGCGCA CCTGCCACCC 720

CTTCACGAGC TGCTCCTTGA GCCTAAAAAG TAGGCTTTAT TCATCCCTTC TGTTCAATTTA 780
CCAACTGGG GGATTGATAC GACCGGGGAA AATGTTCCCTA AACCAGGAAG CTGCGTTAGC 840
GAATCAGCTT TGGTAAGATC TCGCCAACAG CTAGCTGCTT AGGAGTACCC CCACGATACG 900
CACAGCACAC CACTGTCCCT TCACCTGCCT TTCTTCCTGC CTTAGGTAGT TGGGCTTGCC 960
ACCCTAGTTT GCTTTTGTAG TGGTTTGGCA AGGTTAGAAG GCCTCGGCCC CCTCTGTCAT 1020
GCTGGGAAGT GCCTACTCTC TGGGCCACTG CTGCAGAGGC CGTGGCATT GTCATGGGTT 1080
TGGGAAGACCC AGCCATCTGC AGCAGAGGCA GCCTATCCCA TTGCAAGGAG AGGAAGTGA 1140
CGGAGTAATT ATTCTACTCT TCTTTTACA TAAATGGTTT AATTTAAATA ATTCAAAATT 1200
TGAATTTCC TTTACAGAT ACTGATAATC CTTTCCAGTT CTTAAATAAA AACTGCATT 1260
GGATT

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(2) INFORMATION ON SEQ ID NO. 4:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1330 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

```

CTTGAGAGAG CTGGTGGACA TAAAGAAAGG GAATACTCTG CTATTGCAGC ATCTGAAGAG 60
GATCATCTCC GACCTGTGTA AACTCTATAA CCTCCCTCAG CATCCAGATG TGGAGATGCT 120
GGATCAACCC TTGCCAGCAG AGCAGTGCAC ACAGGAAGAC GTGTCTTCAG AAGATGAAGA 180
TGAGGAGATG CTGAGGAGCA CAGAAGACTT AGATCACTAT GAAATGAAAG AGGAGAGGCC 240
AGCTGAGGGC AAGAAATCTG AAGATGATGG CATTGGAAAA GAAACTTGG CCATCCTAGA 300
GAAAAATAAA AAGAACCAGA GGCAAGATTA CTTAAATGGT GCAGTGTCTG GCTCGGTGCA 360
GGCCACTGAC CGGCTGATGA AGGAGCTCAG GGATATATAC CGATCACAGA GTTTCAAAGG 420
CGGAAACTAT GCAGTCGAAC TCCTGGAATGA CAGTCTGTAT GATTGGAATG TCAAACCTCT 480
CAAAGTTGAC CAGGACAGCG CTTTGACAAA CGATCTCCAG ATCCTCAAAG AGAAGAGAGG 540
AGCCGACTTC ATTCTACTTA ACTTTTCCTT TAAAGATAAC TTTCCCTTTG ACCCACCATT 600
TGTCAGGGTT GTGTCTCCAG TCCTCTCTGG AGGGTATGTT CTGGGCGGAG GGGCCATCTG 660
CATGGAACCT CTCACCAAAAC AGGGCTGGAG CAGTGCCTAC TCCATAGAGT CAGTGATCAT 720
GCAGATCAGT GCCACACTGG TGAAGGGGAA AGCAGGAGTG CAGTTTGGAG CCAACAAATC 780
TCAATACAGT CTGACAAAGAC CACAGCAGTC CTACAAGTCC TTGGTGCAGA TCCACGAAAA 840
AAACGGCTGG TACACACCCC CAAAAGAAGA CGGCTAACCC TGGAGTATCA CCGTTCCCTC 900
CTCCCCAGGC ACCACTGGAC CAATTACCTT TGAATGCTGT ATTTGGATCT CACGCTGCCT 960
CTGTGGTTCC CTCCTCATT TTTCTGGAC GTGATAGCTC TGCCTATTGC AGGACAATGA1020

TGCGTATTCT AAACGCTAAG GAAAAAAAC AAACACAGAA CTGTTTCAAG TACTCAAGAC1080
TGACTTACAG AACCAACCA CACCTTGCTG GAACCTTGCG TAGCAGGCAT TCTTATAAAA1140
GAAACTTTCC AGCCTCCTTA TATTGCTGGA AACTCAGCTG TGCTCCAGAC TAGAGCCTCC1200
TTACCTATGC TAGGATTTT TAATTATTT TCTCTTATT CATGTACACT GCTTTTTTTG1260
GTTACAGTGT ATGATGGATG TGTATGAAAA AAATGTATCT TTGGGAAAAC AATTACAGTT1320
TGTTAATTTG                                     1330

```

(2) INFORMATION ON SEQ ID NO. 7:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 762 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

GCGGTCGGTA	GTGCGGCGCT	GTTTAAAGAT	GGCGGCGGAG	GAACCTCAGC	AGCAGAAGCA	60
GGAGCCGCTG	GGCAGCGACT	CCGAAGGTGT	TAACTGTCTG	GCCTATGATG	AAGCCATCAT	120
GGCTCAGCAG	GACCGAATTC	AGCAAGAGAT	TGCTGTGCAG	AACCCCTCTGG	TGTCAGAGCG	180
GCTGGAGCTC	TCGGTCCTAT	ACAAGGAGTA	TGCTGAAGAT	GACAACATCT	ATCAACAGAA	240
GATCAAGGAC	CTCCACAAAA	AGTACTCGTA	CATCCGCAAG	ACCAGGCCCTG	ACGGCAACTG	300
TTTCTATCGG	GCTTTCGGAT	TCTCCCACTT	GGAGGCAC TG	CTGGATGACA	GCAAGGAGTT	360
GCAGCGGTTT	AAGGCTGTGT	CTGCCAAGAG	CAAGGAAGAC	CTGGTGTCCC	AGGGCTTCAC	420
TGAATTCACA	ATTGAGGATT	TCCACAACAC	GTTTCATGGAC	CTGATTGAGC	AGGTGGAGAA	480
GCAGACCTCT	GTGCGCGACC	TGCTGGCCTC	CTTCAATGAC	CAGAGCACCT	CCGACTACCT	540
TGTGGTCTAC	CTGCGGCTGC	TCACCTCGGG	CTACCTGCAG	CGCGAGAGCA	AGTCTTCGA	600
GCACCTTCATC	GAGGGTGGAC	GGACTGTCAA	GGAGTTCTGC	CAGCAGGAGG	TGGAGCCCAT	660
GTGCAAGGAG	AGCGACCACA	TCCACATCAT	TGCGCTGGCC	CAGGCCCTCA	GCGTGTCAT	720
CCAGGTGGAG	TACATGGACC	GCGGCGAGGG	CGGCACCACC	AA		762

(2) INFORMATION ON SEQ ID NO. 8:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1228 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

```

GAAAAATTTC TGAACATGGG TGCACCCCTG GGAGTGGGCC TGGGTCTCGT CTTTGTGTCC 60
TCCATTGGGA TCTATGTTTC TTCCACCTAC CCACCCGTGG CTGGGGCCAC TCTTTACTCA 120
GTGGCAATGT ACGTGGGATT AGTTCITTTT AGCATGTITCC TTCTGTATGA TACCAGAAA 180
GTAATCAAGC GTGCAGAGT ATCACCAGT TATGGAGTTC AAAAAATGA TCCCATTAA 240
TCGATGCTGA GTATCTACAT GGATACATTA AATATATTTA TGCAGATTGC AACTATGCTG 300
GCAACITGGG GCAACAGAAA GAAATGAAGT GACTCAGCTT CTGGCTTCTC TGCTACATCA 360
AATATCTTGT TTAATGGGCG AGATATGCAT TAAATAGTTT GTACAAGCAG CTTTCGTTGA 420
AGTTTAGAAG ATAAGAAACA TGTCATCATA TTTAAATGTT CCGGTAATGT GATGCCTCAG 480
GTCTGCCITT TTTCTGGAG AATAAATGCA GTAATCCTCT CCCAAATAG CACACACATT 540
TTCAATCTCT ATGTTTGAGT GATTTTAAAA TGTTTGGTG AATGTGAAAA CTAAAGTTTG 600
TGTCATGAGA ATGTAAGTCT TTTTCTACT TTAAATTTA GTAGGTTTAC TGAGTAACTA 660
AAATTTAGCA AACCTGTGTT TGCATATTTT TTTGGAGTGC AGAATATTGT AATTATATGT 720
ATAAGTGATT TGGAGCTTTG GTAAAGGGAC CAGAGAGAGG GAGTCACCTG CAGTCTTTTG 780
TTTTTTTAAA TACTTAGAAC TTAGCACTTG TGTTATTGAT TAGTGAGGAG CCAGTAAGAA 840
ACATCTGGGT ATTTGGAAAC AAGTGGTTCAT TGTTACATTC ATCTGCTGAA CTTAACAAAA 900
CTGTTCAATC TGAACAGGC ACAGGTGATG CATTCTCTCG CTGTTGCTTC TCAGTGCTCT 960
CTTTCCAATA TAGATGTGGT CATGTTTGAC TTGTACAGAA TGTTAATCAT ACAGAGAATC1020
CTTGATGGAA TTAATATGT GTTTTITACT TTTGAATGTT ACAAAGGAA ATAACTTTAA1080
AACTATICTC AAGAGAAAAA ATTCAAAGCA TGAATATGT TGCTTTTTC AGAATACAA1140
CATGATACTC ATGAAAAAAA AATGTTTTTT TATTTTGTGA TATTTATTGA ACTGTCTAAT1200
TGAATACAGC TTGCTCTTGT CACCTCAA 1228

```

(2) INFORMATION ON SEQ ID NO. 9:

- (i) SEQUENCE CHARACTERISTIC:
- (A) LENGTH: 914 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

- (iii) HYPOTHETICAL: NO

- (iii) ANTI-SENSE: NO

- (vi) ORIGIN:
- (A) ORGANISM: HUMAN
 - (C) ORGAN:

- (vii) OTHER ORIGIN:
- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

GGCGGTGGTC	CGCCATTTTCG	TGGACGCCGG	GTGAGTGAGA	GAGTTGGTTG	GTGTTGGGCC	60
GGAGGAAAGC	GGGAAGACTC	ATCGGAGCGT	GTGGATTTGA	GCCGCCGCAT	TTTTTAACCC	120
TAGATCTCGA	AATGCATCGT	GATTCCTGTC	CATTGGACTG	TAAGGTTTAT	GTAGGCAATC	180
TTGGAACAA	TGGCACACAG	ACGGAATGCG	AACGGGCTTT	TGGCTACTAT	GGACCACTCC	240
GAAGTGTGTG	GGTTGCTAGA	AACCCACCCG	GCTTTGCTTT	TGTTGAATTT	GAAGATCCCC	300
GAGATGCAGC	TGATGCAGTC	CGAGAGCTAG	ATGGAAGAAC	ACTATGTGGC	TGCCGTGTAA	360
GAGTGGAACT	GTGCAATGGT	GAAAAAAGAA	GTAGAAATCG	TGGCCCACTT	CCCTCTTGGG	420
GTCGTCGCCC	TCGAGATGAT	TATCGTAGGA	GGAGTCCTCC	ACCTCGTCGC	AGATCTCCAA	480
GAAGGAGAAG	CTTCTCTCGC	AGCCGGAGCA	GGTCCCTTTC	TAGAGATAGG	AGAAGAGAGA	540
GATCGCTGTC	TCGGGAGAGA	AATCACAAAG	CGTCCCGATC	CTTCTCTAGG	TCTCGTAGTC	600
GATCTAGGTC	AAATGAAAGG	AAATAGAAGA	CAGTTTGCAA	GAGAAGTGGT	GTACAGGAAA	660
TTACTTCATT	TGACAGGAGT	ATGTACAGAA	AATTCAAGTT	TTGTTTGAGA	CTTCATAAGC	720
TTGGTGCAAT	TTTAAGATGT	TTTAGCTGTT	CAAATCTGTT	TGCTCTTGA	AACAGTGACA	780
CAAAGGTGTA	ATTCTCTATG	GTTTGAAATG	GATCATACGA	GGCATGTAAT	ACCAAGAATT	840
GTTACTTTAC	AATGTTCCCT	TAAGCCAAAA	TTGAATTTGC	TTTGAACCTT	TAGTTATGCA	900
TAGACTGATA	ATAA					914

(2) INFORMATION ON SEQ ID NO. 10:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1126 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

```

GAGGCAGCCC TGACACTATG CCACCTGCTG AGCTCCTGGG TGTCACTAGA GAGCCTCACA 60
CTCTCCTACA ATGGCCTGGG CTCTAACATC TTCCGCGCTG TAGACAGCCT GCGGGGCCCTG 120
TCAGGCCAGG CTGGATGTCG CCTCCGTGCC CTGCATCTCA GTGACCTGTT CTCACCACCTG 180
CCCATCCTGG AGCTGACACG TGCTATCGTG CGAGCACTGC CCCTGCTACG GGTCCCTCTCT 240
ATTGCTGTTG ACCACCCAGG CCAGCGGGAC AACCTGGTG TGCCAGGGAA TGCAGGGCCC 300
CCTAGCCACA TAATAGGCGA TGAGGAGATA CCAGAAAAC TGCCTGGAGCA GTTGGAGATG 360
GGNATTTCAC CCGGGAGCCC AGCCAGCCCC ACTGCTGTGC TCCGTTCTGA AGGCCTCGGG 420
TTCTCTGCAG CAGCTGTCCC TGGATAGTGC CACCTTTGCC TCTCCCCAGG ATTTTGGGCT 480
TGTTTTGCAA ACACTCAAAG AGTACAACCT AGCCCTGAAA AGACTGAGCT TCCATGACAT 540
GAATCTCGCT GACTGTCAGA GCGAGGTGCT CTTTTGCTA CAGAATCTGA CTCTGCAAGA 600
GATTACCTTC TCCTTCTGCC GTCTGTTGA GAAGCGCCCA GCCCAATTTC TGCCTGAGAT 660
GGTTGCTGCT ATGAAGGGCA ACTCCACACT GAAGGCGCTC CGGCTGCCAG GGAACCGCCT 720
GGGGAATGCT GGCCTGCTGG CCTTGCCAGA TGTTCCTCA GAGGATTATC CCTCCTCTCT 780
CTGTCACTG GACATCAGTT CCAACTGCAT CAAGCCAGAT GGGCTTCTGG AGTTCGCCAA 840
GCGGCTGGAG CGCTGGGGCC GTGGAGCCTT TGGTCACTG CGCCTCTTCC AAAACTGGCT 900
GGACCAAGAT GCAGTCACAG CCAGGGAAGC CATCCGGCGG CTCCGGGCTA CCTGCCATGT 960
GGTTAGCGAC TCATGGGACT CATCCAGGC CTTCGCAGAT TATGTTAGCA CCATGTGATG1020
GGGCCCGTAC CTCACAGTCT CATGCTCGGT ACCATCAGT TGCAGGGGCT GAAGCATGGG1080
CTGCCAGAA CCCCACCAC CAGTCTCTATC TTCTCTTTC TGTGAC 1126

```

(2) INFORMATION ON SEQ ID NO. 12:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 538 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

TAGACCACTG	AGGAGACCAT	AGAGCGGATG	CTTTCATGCA	CCCTTTACTG	CACCTTTCTGA	60
CCAGGAGCTA	CTTTGAGTTT	GGTGTACTA	GGATCAGGGT	CAGTCTTTGG	CTTATCAATA	120
AATTTTAACT	TCTGTTAATC	TTACCTGCTT	TAAAAAAAAG	TTCTTGTGTG	TTCGTATCTT	180

TATTTATTC	CTAGTTTGCA	GAAGTGTCTG	AATAAAGGAT	ACAAGGATTA	TTTCAATGTT	240
ACTGCACCTG	AAAACGTGTA	TGTATTAGTG	TGCTAGATTA	TTTAGCAGAA	TATTCACAAG	300
TTTCTGTTGA	CCTTGTTGAT	TGAGCATGAC	TACTAAATAT	TATGTAATAA	AAAGCATTGG	360
TCATAACAGT	CTTATGAAGT	AGTTCCTCGA	ATATAGAAAG	TTCTATAATT	TAGCCCATGA	420
AATGATAGGT	TTTTAATTTT	CAGAAATGGA	GCTGCATGTA	GAATGAGATC	ACATGCTTTT	480
ATATGTGAAA	TATTGGTTTT	AGCAATTAAC	AGAAGGCATA	CTTTGCTAAT	TTTATGGC	538

(2) INFORMATION ON SEQ ID NO. 13:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 321 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

CCCTACAAC	GGTGTCAAAC	TCAGGCTTTC	CCCAGTGACC	AACAATTTTA	ATTCCAAGAG	60
GTGAGGATCT	CAGGAGGTGG	CATTCAACCA	CCAGGGAGCT	AGGGAAGGGG	AACCAAGCTG	120
TCTCCACACC	CAGGAGAGGT	GTCCCTCCAG	CCRAGGCAGG	CAGGACACTC	TGCAGCTCTC	180
CCTCCTGTGC	CCAGGCCCTT	GACTACACTC	TCATCTGCCA	TCTGAGCTAA	GCCAGGAAGG	240
CAGTTAAAGA	AAGGCCCCCA	AACATGAAGC	AGGGACAAGG	AGACGGACAG	GGGTGAGATG	300
ACCCATTGAT	AGGGAAGAGA	G				321

(2) INFORMATION ON SEQ ID NO. 14:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 847 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

TAGACAAATCT	TCTGCATGTC	GGAGGAACGG	GAATTATTCT	GATGAAAAGA	AAGATGCTAT	60
GTATTGGGAA	AAAAGGCGGA	AAAATAATGA	AGCTGCCAAA	AGATCTCGTG	AGAAGCGTCG	120
ACTGAATGAC	CTGGTTTTAG	AGAACAAACT	AATTGCACTG	GGAGAAGAAA	ACGCCACTTT	180
AAAAAGCTGAG	CTGCTTTTAC	TAAAATTAAA	GTTTGGTTTA	ATTAGCTCCA	CAGCATATGC	240
TCAAGAGATT	CAGAAACTCA	GTAATTCTAC	AGCTGTGTAC	TTCAGAGATT	ACCAGACTTC	300
CAAAATCCAAT	GTGAGTTTCA	TTGTGGACGA	GCACGAACCC	TCGATGGTGT	CAAGTAGITG	360
TATTTCTGTC	ATTAAACACT	CTCCACAAAG	CTCGCTGTCC	GATGTTTCAG	AAGTGTCTCT	420
AGTAGAACAC	ACGCAGGAGA	GCTCTGTGCA	GGGAAGCTGC	AGAAGTCCTG	AAAAACAAGT	480
CCAGATTATC	AAGCAAGAGC	CGATGGAATT	AGAGAGCTAC	ACAAGGGAGC	CAAGAGATGA	540
CCGAGGCTCT	TACACAGCGT	CCATCTATCA	AAACTATATG	GGGAATTCTT	TCTCTGGGTA	600
CTCACACTCT	CCCCCACTAC	TGCAAGTCAA	CCGATCCTCC	AGCAACTCCC	CGAGAACGTC	660
GGAACTGAT	GATGGTGTGG	TAGGAAAGTC	ATCTGATGGA	GAAGACGAGC	AACAGGTCCC	720
CAAGGGCCCC	ATCCATTCTC	CAGTTGAACT	CAAGCATGTG	CATGCAACTG	TGGTTAAAGT	780
TCCAGAAAGT	AATTCTCTTG	CCTTGCCACA	CAAGCTCCGG	ATCAAAGCCA	AAGCCATGCA	840
GATCAA						847

(2) INFORMATION ON SEQ ID NO. 16:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 573 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 (A) ORGANISM: HUMAN
 (C) ORGAN:
- (vii) OTHER ORIGIN:
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

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GGAGGCTGCT GGGGGCGGGG CGTCCAGCTC TGGGCCAGGG GSTCCAAAGT GCTCAGCCCC 60
CGGGGACACAG CAGGACGTTT GGGGGCCTTC TTTCCAGCAGG GGACAGCCCG ATTGGGGACA 120
ATGGCGTCTC TTGGCCACAT CTTGGTTTTT TGTGTGGGTC TCCTCACCAT GGCCAAGGCA 180
GAAAGTCCAA AGGAACACGA CCCGTTCACT TACGACTACC AGTCCTGCA GATCGGAGGC 240
CTCGTCATCG CCGGGATCCT CTTTCATCTG GGCATCCTCA TCGTGCTGAG CAGAAGATGC 300
CGGTGCAAGT TCAACACAGCA GCAGAGGACT GGGGAACCCG ATGAAGAGGA GGGAACTTTC 360
CGCAGCTCCA TCCGCCGTCT GTCCACCCGC AGGCGGTAGA AACACCTGGA GCGATGGAAT 420
CCGCCAGGA CTCCCTGGC ACCTGACATC TCCCAGGCTC CACCTGCGCG CCCACGGGCC 480
CCTCCGCCGC CCCTTCCCCA GCCCTGCCCC CGCAGACTCC CCCTGCCGCC AAGACTTCCA 540
ATAAAACGTG CGTTCCTCT GACAAAAAAA AAA 573

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(2) INFORMATION ON SEQ ID NO. 17:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 486 base pairs
 (B) TYPE: Nucleic acid
 (C) STRAND: individual
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 (A) ORGANISM: HUMAN
 (C) ORGAN:
- (vii) OTHER ORIGIN:
 (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

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CCCCGACGGC TTGCTGGGGC TGGGCTCTTC CTCGCGGAAG TGGGGAGGAG GCGGTTGCGG 60
TTAGTGGACC GGGACCGGTA GGGGTGCTGT TGCCATCATG GCTGACCCCG ACCCCCGGTA 120
CCCTCGCTCC TCGATCGAGG ACGACTTCAA CTATGGCAGC AGCGTGGGCT CCGCCACCGT 180
GCACATCCGA ATGGGCTTTC TGAGAAAAGT CTACAGCATT TTTTCTCTGC AGGTTCTCTT 240
AACTACAGTG ACTTCAACAG TTTTTTATA CTTTGAGTCT GTACGGACAT TTGTACATGA 300
GAGTCCTGCC TTAATTTTGC TGTTTGCCCT CGGATCTCTG GGTTTGATT TTGCGTTGAC 360
TTTAAACAGA CATAAGTATC CCCTTAACCT GTACCTACTT TTTGGATT TA CGTGTGTTGA 420
AGCTCTGACT GTGGCAGTTG TTGTTACTTC TATGATGTAT ATATTATCTG CAAGCTTTCA 480
TACTGA 486

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(2) INFORMATION ON SEQ ID NO. 18:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 662 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

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CTTTTTCCT CTACTCCTTC CCCTTCACAC CCCCCTGGCT GGAAGGAACC TCGGCTTCCC 60
TGAAAGCTTG GGGGTCCAC CTTTCTTACC CCACCCGGGA GGAACGCCA GGGCCCCGGG 120
CTTGTTCCTC CTCTTGTTTT CTTTGGGGC AGTTTGATCA CTGATCGAGT AAGGAATGAC 180
CTTTAGATTG TGCAGCTTTT GTTTTGTGTT TTTTAAATT TTTTAAACCA AGAATGATT 240
CTCCTGCTTC CTCTCCTCA CCATCTTCCC AGACGGAGT CAAAGGCCAC TTCTCAAGCA 300
GCTTTTGGA CTTTCAGCCT CAGAGTGAA TCCTTTAAAG ACAGGACCCC TATGTCCAGG 360
AAAGGGGAAA AGGAACCTTG CCAATGATAG TGACACAGC AAAAGCAATA AAATAATAAA 420
ATAAAAAACA ATAGCACAGC CTTTGTGAG GTACAGAGG AGGAGGGGCT GCCCGGAGT 480
GGGTCCCTGC CTGGATTTG ACACAGCAAC TTCTGTAGT GAGCACTTG TATGAATCGT 540
GGACTTCCTG TTCTCAAGGC GCAGGTATT ATTCTGTAT TGTCTAGAG ACACACCAA 600
ATCCAACCTT CTAATAACA TGATGGCGCA GTCCCAAAA AGGAACAGA AGAAGAAAAG 660
GG 662

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(2) INFORMATION ON SEQ ID NO. 19:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 750 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

ATAGATTTTG	AGGGGAAGGA	GAGAGGGAAG	GGTCAGGGTA	GAGACACCCC	TCCCTTGCCC	60
CTTTCCTGGG	CCCAGAAGTT	GGGGGGAGGG	AGGGAAAGGA	TTTTTACATT	TTTAAACTG	120
CTATTTTCTG	AATGGAACAA	GCTGGGCCAA	GGGGCCCAGG	CCCTGTCCCTC	TGTCCTCCAC	180
ACCCCTTTGC	TCCGTTTCAT	CATTCAAAAA	AACATTCTCT	GAGCACCTTC	TGTGCCCAGC	240
ATATGCTAGG	CCCACCAGCT	AAGTGTGTGT	GGGGGGTCTC	TACGCCAGCT	CATCAGTGCC	300
TCCTTGCCCA	TCCTTCACGG	GTGCCCTTGG	GGGATCTGTA	GGAGGTGGGA	CCTTCTGTGG	360
GGTTTGGGGA	TCTCCAGGAA	GCCCGACCAA	GCTGTCCCCT	TCCCTGTGTC	CAACCCATCT	420
CCTACAGCCC	CCTGCCTGAT	CCCCTGCTGG	CTGGGGGCAG	CTCCCAGGAT	ATCCTGCCTT	480
CCCAACTGTT	CTGAAGCCCC	TCTCCTTAAC	ATGGCGATTG	CGGAGGTCAA	GGCCTTGGGC	540
TCTCCCCAGG	GTCTAACGGT	TAAGGGGACC	CACATACCAG	TGCCAAGGGG	GATGTCAAGT	600
GGTGATGTCG	TTGTGCTCCC	CTCCCCCAGA	GCGGGTGGGC	GGGGGGTGAA	TATGTTGGC	660
CTGCATCAGG	TGGCCTTCCC	ATTTAAGTGC	CTTCTCTGTG	ACTGAGAGCC	CTAGTGTGAT	720
GAGAACTAAA	GAGAAAGCCA	GACCCCTAAA				750

(2) INFORMATION ON SEQ ID NO. 21:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1001 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

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GGGGGGAGAGA GGGAGGCCTT TGGGCGGTGG GGGCCACGGG GAGGGTGGTC CTCGGACTAC 60
GTGCGGGGACA GGAGGTCAGG GCTGGCAAGT CCCTCAGGCC TCCCTCGTTG CCCCAGCCTC 120
GCGGGCCGCC TAACTGCCCC GTTCCAAGGG TGCCACCGGA CCCCCTGGA GAGGAAGTTC 180
TCCGTTGGCT GATTTCATCA CCACCCATTC CCGATTCCAC GTTTCCTTTA AGCGGGGCTG 240

CGCGAGCGCA AGGGGGCAAG GAACTGGATT GCGATTGGTC AGCACGTGCC TCGGTCGGCG 300
GTACAATTGG CTGAGGCGCT GGGCCTTGGG AAGCATTCCT CGACGGGATT GGTGCTCGCT 360
CTCGCAGAGC CCGCTCCCGC CAGTACAAGC GGCCCCCGGG TGGGGGGGGA GGAGGGGACT 420
CCGGGAGGAG GAACATGGCG GTGGCGGACC TCGCTCTCAT TCCTGATGTG GACATCGACT 480
TCGACGGCGT TTCAAGTAT GTGCTGATCC GAGTCCACTC GGCTCCCGCG TCGGGGGCTC 540
GGGCTGCAGA GAGCAAGGAG ATCGTGCGCG GCTACAAGTG GGCTGAGTAC CATGCGGACA 600
CTACGACAA AGTGTCGGCG GACATGCAGA AGCAAGGCTG CGACTGTGAG TGTCTGGGCG 660
CGCGGCGCAT CTCCCACCAG ACTCAGGACA AGAAGATTCA CGTGTACGGC TATTCCATGG 720
CTTATGGTCC TGCCCAGCAC GCCATTTCAG CTGAGAAAAT CAAAGCCAAG TACCCCGACT 780
ACGAGCTCAC CTGGGCTAAC GACGGCTACT GAGCACTCCC AGCCCCGGGC CTGCTGCCTC 840
CAGCAGCCAC TTCAGAGCCC CCGCCTTTGC CTGCACTCCT CTGTCAGGGC TGCCCGTGCC 900
TGCTCCTGCG GCAGCCTCTG GTGACGTGCT GTCCACCAGG CCTTGGAGAC AGGCTAGCCT 960
GGCCACAGAA TTAAACGTGT TGCCACACCT GCCGGCTTCT G 1001

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(2) INFORMATION ON SEQ ID NO. 23:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 580 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

CGAAACGTGC	GCAGGCGCCG	GCCGCTGCGC	TGCAGATGGC	GGAAATGGAT	CCGGTAGCCG	60
AGTTCCTCCCA	GCCTCCCGGT	GCTGCGCGCT	GGGCTGAGGC	CCTTCTGCGA	TGTTTTACCT	120
GGCTGCGGCT	GTGTCAAGAT	TCTATGTTCC	TGTCTCTGAA	ATGCCTGAAC	ACAAGATCCA	180
GTCACTCGGG	GGCCCACTGC	AGATAACAAT	GAAGATGGTG	CCAAAACCTG	TTTCTCCTTT	240
GGTTAAAGAT	TGGGCTCCCA	AAGCATTTAT	AATTTCTCTT	AAGTTGGAGA	CTGACCCCGC	300
CATTGTAAAT	AATCGAGCTC	GGAAGGCTTT	GGAAATTTAT	CAGCATCAAG	TGGTGGTGGC	360
TAATATCCTT	GAGTCACGAC	AGTCCTTTGT	GTTTATTGTA	ACCAAAGACT	CGGAAACCAA	420
GTTATTGCTA	TCAGAGGAAG	AAATAGAAAA	AGGCGTAGAG	ATAGAAAGAG	AGATAGTGGA	480
TAATCTTCAG	TCTCGACACA	CAGCTTTTAT	AGGTGACAGA	AACTGAAGTA	AAAAGCCCTT	540
ATAGGATCAA	AAATTGTTCA	GGGCTCTTAG	AGATGGTGAA			580

(2) INFORMATION ON SEQ ID NO. 24:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 740 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

GGATGCGTGG	CGGGGAGCGC	CGGGCTCTCC	CGGAAGTCTC	CCTGGACGGA	AGTGGAAACG	60
GAAACCTTTT	TAGGGAGTCC	AAGGTACAGT	CGCCGCGTGC	GGAGTTGTGA	CTGGTTACTT	120
GGCCTCATGG	CGGTCCGAGC	TTCTGTCGAG	AACAACCTGT	AGATCGGCTG	CTTTGCCAAG	180
CTCACCAACA	CCTACTGTCT	GGTAGCGATC	GGAGGCTCAG	AGAACTTCTA	CAGTGTGTTC	240
GAGGGCGAGC	TCTCCGATAC	CATCCCCGTG	GTGCACGCGT	CTATCGCCGG	CTGCCGCATC	300
ATCGGGCGCA	TGTGTGTGGG	GAACAGGCAC	GGTCTCTTGG	TACCCAACAA	TACCACCGAC	360
CAGGAGCTGC	AACACATTTC	CAACAGCCTC	CCAGACACAG	TCCAGATTAG	CGGGGTGGAG	420
GAGCGGCTCT	CAGCCTTGGG	CAATGTCACC	ACCTGCAATG	ACTACGTGGC	CTTGGTCCAC	480
CCAGACTTGG	ACAGGGAGAG	AGAAAGAAAT	CTGGCAGATG	TGCTCAAGGT	GGAAGTCTTC	540
AGACAGACAG	TGGCCGACCA	GGTGCTAGTA	GGAAGCTACT	GTGTCTTCAG	CAATCAGGGA	600
GGGCTGGTGC	ATCCCAAGAC	TTCAATTGAA	GACCAAGGATG	AGTGTCTCTC	TTTTCAAGTC	660
CCTTGTGGCG	GGGATGTGAA	CGAAGCATTA	AGTGATTCTT	GGGATGTGTA	TAATGTGTCC	720
TTCTGTCCTG	AAACCACCA					740

(2) INFORMATION ON SEQ ID NO. 26:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 975 base pairs
 (B) TYPE: Nucleic acid
 (C) STRAND: individual
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 (A) ORGANISM: HUMAN
 (C) ORGAN:
- (vii) OTHER ORIGIN:
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

ATGGGCTACA	ACCTGAGCCC	CCAGTTCACC	CAGCTTCTGG	TCTCCCGCTA	CTGCCACGC	60
TCTGCCAATC	CTGCCATGCA	GCTTGACCGC	TTCATCCAGG	TGTGCACCCA	GCTGCAGGTG	120
CTGACAGAGG	CCTTCCGGGA	GAAGGACACA	GCTGTACAAG	GCAACATCCG	GCTCAGCTTC	180
GAGGACTTCG	TCACCATGAC	AGCTTCTCGG	ATGCTATGAC	CCAACCATCT	GTGGAGAGTG	240
GAGTGCACCA	GGGACCTTTC	CTGGCTTCTT	AGAGTGAGAG	AAGTATGTGG	ACATCTCTTC	300
TTTTCTCTGC	CCTCTAGAAG	AACATTCTCC	CTTGCTTGAT	GCAACACTGT	TCCAAAAGAG	360
GGTGGAGAGT	CCTGCATCAT	AGCCACCAAA	TAGTGAGGAC	CGGGGCTGAG	GCCACACAGA	420
TAGGGGCTTG	ATGGAGGAGA	GGATAGAAGT	TGAATGTCCT	GATGGCCATG	AGCAGTTGAG	480
TGGCACAGCC	TGGCACCAGG	AGCAGGTCCT	TGTAATGGAG	TTAGTGTCCTA	GTCAGCTGAG	540
CTCCACCCCTG	ATGCCAGTGG	TGAGTGTTC	TCGGCCTGTT	ACCGTTAGTA	CCTGTGTTCC	600
CTCACCAGGC	CATCCTGTCA	AACGAGCCCA	TTTTCTCCAA	AGTGAATCT	GACCAAGCAT	660
GAGAGAGATC	TGTCTATGGG	ACCAGTGGCT	TGGATTCTGC	CACACCCATA	AATCCTTGTG	720
TGTTAACTTC	TAGCTGCCTG	GGGCTGGCCC	TGCTCAGACA	AATCTGCTCC	CTGGGCATCT	780
TTGGCCAGGC	TTCTGCCCTC	TGCAGCTGGG	ACCCCTCACT	TGCTGCCAT	GCTCTGCTCG	840
GCTTCAGTCT	CCAGGAGACA	GTGGTCACCT	CTCCCTGCCA	ATACTTTTTT	TAATTTGCAT	900
TTTTTTTCAT	TGGGGGCCAA	AAGTCCAGTG	AAATTGTAAG	CTTCAATAAA	AGGATGAAAC	960
TCTGGA AAAA	AAAAA					975

(2) INFORMATION ON SEQ ID NO. 27:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 854 base pairs
 (B) TYPE: Nucleic acid
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

GAACACACAC	ACAGGTGTTT	TGACCAGCTC	AGGCTTGCCA	CAGTGAGCAA	CTCTGTGGCT	60
AGCAAAAGAG	AAGTTTATTT	GTGCCCAGCC	ATTGGTCACC	TTGGGTGATG	CACCAGATAG	120
CAGGCAGATG	TGGTTCATT	GGCCTTCGTC	CTCTTTCCTC	CTAAAATAAT	ATTGGCTTTA	180
CCATCTTAAC	TCAGCTGTGG	GTTTTTTGTG	GGTTCTTGTT	TGTTTTTTGG	CATGAATTGT	240
CATCTTTGGT	GTTTTTTTAA	CCCCCAGCCC	CTCAAAAAAA	TAAGGCCTCC	AGGTATCAAG	300
ATCTCATATT	AGGATTTTCT	GTCCTTAATT	TTTGAGCAA	AATCTGGAAA	ATGTGAAAGC	360
ATATTTAGAT	TTTATATACT	ATCTGAAATG	TGATTTGTTA	AGATTCCTTA	ATTTGGGCCT	420
CTTAGAATAA	TTTTGAATGA	GATCTACCGA	CTCACTTGTC	AGATATTTTT	TCACAGATTA	480
CTCTTGGGCC	TTTTCATTAG	AAAGCTGTTT	GTTTGTCCTC	CTGTTGTGTC	ATTTGGTTAC	540
CTCATTTTGC	CGTTTCAGAT	TGTGAAAGCT	CACAGGGGTG	TTTTTTGGAA	TCATTTGCTG	600
AGTCATTTTC	TCAAAATCAT	TTCCATTGTA	TCAGTTAACA	TATAGTTTTA	AATGTATGTA	660
TTATAAATAT	CTGTAACCAA	ATCATTTGAA	GGCTTGATAA	ATTTTAAACA	AAGTTTGTAC	720
ATTTTTTATG	AAAGTTACTA	GTAATGCTTT	ACTAAGTAGT	GCAATGAATT	TTTATTTTTA	780
ATCCCTGTGC	CCAATTTTGG	AGTTGAGAGG	GTTGTTGGTA	ATAAATGTAT	GATGTACACT	840
TAATAAAAAA	AAAA					854

(2) INFORMATION ON SEQ ID NO. 28:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 802 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

TTTTTTTCAG	AGTGTAGGG	CTTTATTACA	AATGGAGTTG	ACTGCTAGAG	AGGCCCTTCT	60
CCAATCTTTC	TTCTGTACCT	TCTTCCCTCC	CAAAGACATC	CCTCTAGGGG	AGGTCACTAG	120
GCCATTAGGT	AGGAGGAAAT	CTGGAGAGTG	AAAAGGGGCC	TTGCTTTTGT	CAAAGTCCTC	180
TGAAACAACC	ACTGAGTCTG	AAGGCTGGCT	CCAGTTGAGA	ATCTTCTAGT	GGAAAGAGGT	240
TAGCTCTCAT	CTTCAAGGTC	CTTCATTCTT	ACATCCCTGG	GGGCTTTTGT	CTTCTTTTGC	300
CTTTTGAGCT	GTGGTTCACT	AGTCCTGGCT	GGCTTTGAAG	GGGCTTCCAC	TTCCATGGCT	360
GTCTTCTCTT	TCTGGGCAAG	CCGGATCTGC	TGGAGGAGTT	TTCTGCGCTT	CTTCCCTGAC	420
AGTGTAATGT	TGGCAGCTGC	ACTGGACGCC	CGCTTCTTGA	GGTGGTGCCG	CGTGATCAGC	480
CCTTGGTCTA	TCACAGCCCC	GACCACCCGG	TGCCTCAGAC	GCCGCTCCCG	ATTCAACACC	540
CGCCGGCGTT	TGAACAGCTT	CTTCTTCAGC	TCCGTTCCGG	GCCGTTGAT	CTTCCCCCCC	600
GGAGCTCCCA	TAGTCGCGAT	TCCACTCCAG	TTCACGCTCC	GTACTTCCGC	TCAGCGCCGG	660
ATCCGCGGGC	TCCGCCCCGG	CTTCCCGGG	GCCAATCGCA	ACTCGGGGGC	GGGTCTCTCG	720
CTATATAAAA	GGAGCTCCSC	GGTCCGGGAG	GCCTTTCGGA	GGGTGGTGAG	CTAGTAAGTG	780
GGTTTTAGC	TGTAGTAGCC	AG				802

(2) INFORMATION ON SEQ ID NO. 29:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 807 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

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CCCCGTCGCG GCGTGGTGGC TGCTGCTGTG CATGTCCCCTG CGATGGGAGT CTTGTGCCCC 60
GCCTGTCACT TTCTCCCCA GGGCAGAGCT CCCCTTCCTG CAAGAGTCTG GGAGGCGGTG 120
CAGGCTGTCC TGGCTGCTCT GGGGAAGCCG AGGGACAGCC ATAACACCCC CGGGACAGTA 180
GGTCTGGGCG GCACCACTGG GAACTCTGGA CTTGAGTGTG TTTGCCTCTT CCTTGGGTAT 240
GAATGTGTGA GTTCACCCAG AGGCCTGCTC TCCTCACACA TTGTGTGGTT TGGGGTTAAT 300
GATGAGGGA GACACCTCCT CATAGACGGC AGGTGCCAC CTTTCAGGGA GTCTCCCAGC 360
ATGGGCGGAT GCCGGGCATG AGCTGCTGTA AACTATTTGT GGCTGTGCTG CTTGAGTGAC 420
GTCTCTGTCT GTTGGGTGCC AAGTGCTTGT GTAGAACTG TGTCTGAGC CCCCTTTTCT 480
GGACACCAAC TGTGTCTCTG GAATGTATCG CTACTGTGAG CTGTTCCCGC CTAGCCAGGG 540
CCATGTCTTA GGTGCAGCTG TGCCACGGGT CAGCTGAGCC ACAGTCCCAG AACCAAGCTC 600
TCGGTGTCTC GGGCCACCAT CCGCCCCACT CGGGCTGACC CCACCTCCTC CATGGACAGT 660
GTGAGCCCCG GGCCGTGCAT CCTGCTCAGT GTGGCGTCAG TGTCCGGGCT GAGCCCTTG 720
AGCTGCTTCA GTGAATGTAC AGTGCCCGGC ACGAGCTGAA CCTCATGTGT TCCACTCCCA 780
ATAAAAGGTT GACAGGGAAA AAAAAAA 807

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(2) INFORMATION ON SEQ ID NO. 30:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 777 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

CTCTCTGCCA	GCTGATGTGC	CCTGTTGCC	CCCACCCCAT	CCCGCACAGA	ACCATCCCTG	60
CATTCCACAG	GGGACTCGGG	CAAGGGTGCC	GAAGATAGAC	AAGAGGCACA	CAGAGACAGA	120
CCAAC TGCCA	GCCAGGCAGC	CCCAGAGGAG	AGAGACATTC	AGACAGAGGA	AAGTCTCCCT	180
GCCCCTCATT	CCTTCCAAGA	TGAGAAAAAC	TTGCCGCCAC	CCCCCGACAC	TGATGCCAGG	240
GAGGTGGGAG	GAAGAAGTGG	GAAATTTCCT	TTCCAGTAC	CCCCAAGAAC	GTCTGAGCCT	300
TCAATTTTGA	ATTTTTTCTT	TATTAATAAT	ACTTTTATCT	TATAAATCA	ACTAATCAAA	360
AATGATATAG	ACGACAGCAC	TGGCTCTGTG	AAGGTGGCAT	CTTCTGGGG	AGGCAGGCCA	420
TGGGGCATGG	AGGAGGGTGC	AAAGATATGG	GTTGCTGTCT	TCTGGCCTCC	AGCTGCATGG	480
AGGCCGGCCC	AGGGTCTAGG	GTGTGCACTG	GGCAAGGGCA	GGCGGCAGG	TGTCAGGCCG	540
GCTTGGACAA	TGAAACCCCTG	ACCTTGCTGC	ATTCCCTTTT	CTCCACCAC	CACTAGCTTC	600
TTTGGAACTC	TGGGGTGGGG	GTCACTTTTG	GGGATTATGG	CTGCCACCCG	GGATTTGAGT	660
GTAGGGAGTG	TGGGAGCAGC	CTTGGCAGAT	GGGCAACCCG	TGCCCTGCAG	GTGTTGACAA	720
GATCCGCCAT	CTGTAATGTC	CTTGGCACAA	TAAACCAAAA	TGTCAGTTTC	AAAAAAA	777

(2) INFORMATION ON SEQ ID NO. 31:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 501 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

CCGATTCGG	CCCCGCCCGC	TGGATCCGG	TTCCGCTCCC	CACAACCCGC	TCTGTGGCGG	60
GGCTTCGGT	CGGGAGGGTC	CGCCAGCTCT	CGCGTCCTTT	GCTGGGTCCA	GACACCGGTT	120
CCGTTGCAAA	CATTTTTTAA	GGGCTGTTA	TTCTTCTGTA	AATGAGTTTG	GTGATTAGAA	180
ATCTGCAGCG	AGTCATCCCC	ATCAGGAGAG	CGCCACTTCG	CAGTAAGATC	GAGATTGTAA	240
GGAGGATTT	AGGAGTGACG	AAATTTGACC	TGGGGATCAT	CTGTGTTGAC	AACAAGAAATA	300
TTACGACAT	TAATAGAATC	TACAGAGATA	GAAATGTCCC	AACCGATGTG	CTTTCTTTTC	360
CATTTTATGA	GCATCTGAAA	GCAGGTGAAT	TTCCCGAGCC	TGATTTTCCA	GATGACTACA	420
ATTTGGGAGA	CATTTTCTTA	GGAGTGGAGT	ATATCTTCCA	TCAGTGTAGA	GAAGATGAAG	480
ATTACAATGA	CGTCTGACT	G				501

(2) INFORMATION ON SEQ ID NO. 32:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1104 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

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ATTTTGACCC TAAACTTTTG GAAGGAAAAG TAAAGGAGGA TCCTGACCAG GGGGAATCCA 60
TGAACCTTTT AACCTTTTGA AGGTTCTACT TGCCAATTCT GGTTCCCAGC GCAAAGAAGG 120
CCATATACAT GGATGATGAT GTAATTGTGC AAGGTGATAT TCTTGCCCTT TACAATACAG 180
CACTGAAGCC AGGACATGCA GCTGCATTTT CAGAAGATTG TGATTCAGCC TCTACTAAAG 240
TTGTTCATCCG TGGAGCAGGA AACCAGTACA ATTACATTGG CTATCTTGAC TATAAAAAGG 300
AAAGAATTCTG TAAGCTTTC ATGAAAGCCA GCACTTGCTC ATTTAATCCT GGAGTTTGTG 360
TTGCAAACTT GACGGAAATG AAACGACAGA ATATAACTAA CCAACTGGAA AAATGGATGA 420
AACTCAATGT AGAAGAGGGA CTGTATAGCA GAACCTTGGC TGGTAGCATC ACAACACCTC 480
CTGTGCTTAT CGTATTTTAT CAACAGCACT CTACCATCGA TCCTATGTGG AATGTCCGCC 540
ACCTTGGTTC CAGTGCTGGA AAACGATATT CACCTCAGTT TGTAAAGGCT GCCAAGTTAC 600
TCCATTGGAA TGGACATTG AAGCCATGGG GAAGGACTGC TTCATATACT GATGTTTGGG 660
AAAAATGGTA TATTCACAG CCAACAGGCA AATTCAACCT AATCCGAAGA TATACCGAGA 720
TCTCAACATC AAAGTGAAC AGAATTGTA CTGTAAGCAA GCATTTCTCA GGAAGTCCTG 780

GAAGATAGCA TGCCTGGGAA GTAACAGTTG CTAGGCTTCA ATGCCTATCG GTAGCAAGCC 840
ATGGAAGGAG ATGTGTCAGC TAGGTAAAGA TGACAACTG CCCTGTCTGG CAGTCAGCTT 900
CCCAGACAGA CTATAGACTA TAAATATGTC TCCATCTGCC TTACCAAGTG TTTTCTTACT 960
ACAATGCTGA ATGACTGGAA AGAAGAAGTG ATATGGCTAG TTCAGCTAGC TGGTACAGAT 1020
AATTCAAAC TGCTGTGGT TTTAATTTTG TAACCTGTGG CCTGATCTGT AAATAAACT 1080
TACATTTTTC AAAAAAAAAA AAAA

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1104

(2) INFORMATION ON SEQ ID NO. 33:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 810 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

GCCATCCTTT	ATCATCCACA	GCAATCCCAT	CTGGTTGGGA	GCACTGCTCT	GGGTCTCACA	60
CTGCCCTCC	TCTATCCTAG	GGAGCCTGAG	GCCCAGGGGT	GAAAAGATCC	AGTTGCGGGT	120
GGGGGGTAGT	GAACCGTGCA	GGATAATGAA	AGCAACTGTC	TTTGGAAATG	ACCTACCGCT	180
ACCCGTTGTC	TGAGACTGAG	ATTATCTCAG	ACTGTCTTCT	GGCTTCTGCC	AAAACACTCC	240
CTTAACAGAA	AGCACCAGG	GGATGGGGGT	AGGGGGGTG	GGGAGAGTGA	GGCTTGAGTG	300
TGAAGGAAGT	CTCATATATG	CAGAGCTGAA	ATCTCCCTCT	TTGTATGTCC	ACACTTTTGT	360
CTGTGTTCTCT	AGACTGATTC	TTGCTATTCC	AAATCCTCTT	CCACGTTGAC	AGCCCTTCAG	420
ATATTTCAAC	ACTCCTCTCA	GCATCCTCCA	CTTCCCCCAT	CTCTCCAAGC	TGAACCTTGGT	480
TCACAGGGTG	GGATTGTGTA	TGTGCATGCA	GGAGGTGGGG	GTGGACAGTG	CCCTGGGCTG	540
GAATCCCCCT	TAGTTCTAAG	TGCCTCCTTG	CCCCGAGCTT	CGAGAGCTGT	GCCCAGGAGT	600
GAACRACCAG	CCCTACCTCT	GTGAGAGTGG	TCACTGCTGC	GGGGAGACTG	GCTGCTGCAC	660
CTACTACTAT	GAGCTCTGGT	GGTTCTGGCT	GCTCTGGACT	GTCTCATCC	TCTTTAGCTG	720
CTGTTGCGCC	TTCCGCCACC	GACGAGCTAA	ACTCAGGCTG	CAACAACAGC	AGCGGCACGT	780
GGAAATCAAC	TTGTTGGCCT	ATCATGGGGC				810

(2) INFORMATION ON SEQ ID NO. 35:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 826 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 (A) ORGANISM: HUMAN
 (C) ORGAN:
- (vii) OTHER ORIGIN:
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

TGGAAATCAT	GGCAACTACA	CAGGATGTTG	CTTACCAGGA	CGGAGTTTGT	GTATCTTAGT	60
ACTGAAGTTA	GCACATGTTT	TACATGCAAA	AGATTAAGGA	AAAAACCCCTT	AAAGTGGACA	120
GGTATCCAAA	GTTTCATTTT	TGTGACTCAT	CAAAGTGACA	AAAGACTTGT	AACAACTTTG	180
CCTGGACTTT	TTTCATTTTA	CAACAGTTCA	TCCATTACACA	ATGATTTTGT	TCTCTGCTCC	240
ATATTTTTTA	ATCCCTTAAG	CATTTGATGA	AACACTCTTT	AGTGTATAT	GCATTTTCTT	300
ACTTTTGTTA	AAAATGTGAC	AATTGTCAAA	AAATGCACTA	AAATGTAAAT	GGAGATTGAA	360
CAAGTTCAC	TTCCAGCTTA	TAGGCAACTT	TATACAGACT	TGAACATTTT	CTCCAGTTGT	420
TTAGTAAAAG	TGAAGAGAA	AGGTTTTTTC	CTGCCACAGG	ATATAACTTT	TTTTTATATA	480
ACAAGCATAA	CACACCAC	CTTTTGGTGG	AAAAGTGCAG	AATAGTATGT	ACCTTTTATG	540
AAGAAAAATG	TAATTTACAA	TATTCAGTGA	GAATGTTACT	GCTGATTTTC	TTTTCCAAGG	600
TGTAGAATAT	TCCTTGATTT	ATAGAATTCA	TTTTTGACCC	AGATGATGGT	TCCTTTACAG	660
AACAATAAAA	TGGGTGAACA	TTTTCACAAA	TAGAGTGTA	CGAAGTCTGG	ATTTCTGATA	720
CCCTTGTCATT	TGGGGGATTT	TATTTTACTT	TGTTGCTTTA	AAATTCAATG	CAGAGAGTT	780
GTGTACTGTA	GGGGAATAA	AGTTAATTCA	AATTTGAAA	AAAAAA		826

(2) INFORMATION ON SEQ ID NO. 36:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 578 base pairs
 (B) TYPE: Nucleic acid
 (C) STRAND: individual
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 (A) ORGANISM: HUMAN
 (C) ORGAN:
- (vii) OTHER ORIGIN:
 (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

GTCTTAACT	GTTCCATTTT	CCGTATCTGC	TTCGGGCTTC	CACCTCATTT	TTTTGCTTT	60
GCCCATCTG	TTTCAGCCAG	TCGCCAAGAA	TCATGAAAGT	CGCCAGTGGC	AGCACCGCCA	120
CCGCCGCCGC	GGGCCCCAGC	TGCGCGCTGA	AGGCCGGCAA	GACAGCGAGC	GGTGCGGGCG	180
AGGTGGTGGC	CTGTCTGTCT	GAGCAGAGCG	TGGCCATCTC	GCCTGCGGCC	GGGGGCGCCG	240
GGGCGCGCCT	GCCTGGCCCTG	CTGGACGAGC	AGCAGGTAAA	CGTGCTGCTC	TACGACATGA	300
ACGGCTGTTA	CTCAGCCCTC	AAGGAGCTGG	TGCCACCCTT	GCCCCAGAAC	CGCAAGGTGA	360
GCAAGGTGGA	GATTCTCCAG	CAGCTCATCG	ACTACATCAG	GGACCTTCAG	TTGGAGCTGA	420
ACTCGGAATC	CGAAGTTGGA	ACCCCCGGGG	GCCGAGGGCT	GCGGGTCCGG	GCTCCGCTCA	480
GCAACCTCAA	CGGCGAGATC	AGCGCCCTGA	CGGCCGAGGC	GGCATCGCTT	CCTGCGGACG	540
ATCGCATCTT	GTGTCGTGA	AGGCCTCCCC	CAGGGACC			578

(2) INFORMATION ON SEQ ID NO. 37:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 799 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

AGCTTTTGT	CACACTTTAA	ATAGCAGTCC	CAGAATGATT	TCACTACAGA	CTCTCTGGAA	60
AGCCTGGGAG	CTGAATTCGG	GAAGATCCCC	ACATCGATGA	AAGCAAAGCG	AAGCACCAAG	120
CCATCATCAT	GTCCACGTCG	CTACGAGTCA	GCCCATCCAT	CCATGGGTAC	CACCTTCGACA	180
CAGCCTCTCG	TAGAAAGGCC	GTGGGCAACA	TCTTTGAAAA	CACAGACCAA	GAATCACTAG	240
AAAGGCTCTT	CAGAACTCT	GGAGACAAGA	AAGCAGAGGA	GAGAGCCAAG	ATCATTTTGT	300
CCATAGATCA	AGATGTGGAG	GAGAAAACGC	GTGCCCTGAT	GGCCTTTGAAG	AAGAGGACAA	360
AAGACAAGCT	TTTCCAGTTT	CTGAAACTGC	GGAAATATTC	CATCAAAGTT	CACTGAAGAG	420
AAGAGGATGG	ATAAGGACGT	TATCCAAGAA	TGGACATTCA	AAGACCAAGT	GAGTTTGTGA	480
GATTCTAACA	GATGCAGCAT	TTTGCTGCTA	CCTTACAAGC	TTCTCTTCTG	TCAGGACTCC	540
AGAGGCTGGA	AAGGGACCCG	GACTGGAAAG	GGACCAGGAC	TGAACAGACT	GGTTACAAGG	600
ACTCCAACA	ATTTTCATGCC	CTGTGCTGTT	ACAGAGGAGA	ACAAAATGCT	TTACAGCAAGG	660
ATTTGAAAAC	TCTTCCGTCC	CTGCAGGAAA	GGATTGACGC	TGATAGAAGA	GCCTGGACAG	720
ATGTAATGAG	AACTAAAGAA	AACGATGGCT	GGAGATGACA	TTTATCCAGG	GTCACCTTGT	780
CAGGCCCTAG	GACTTAAAT					799

(2) INFORMATION ON SEQ ID NO. 39:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1743 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

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AATTTATTTT TTTTTCATGG TCTGTCAGGT TTTATTTATA GAGTCTGGTG AACTTGAAGT 60
AGAGAAAAGCT GCAAAAAGTGT GTTTGAGAG CATGGCAGGG CCATGGAGAA GGGCTAATAG 120
AAGCAGGTCC CTTCGCCAGA CCTTCAGGGA GCCCTTTTGG TGGATAGCGG ACACCTGAGG 180
CAGGAGGTGG CAGGGGCCAA GTCCAGGCAG GCAGCAGCAG GGCTGCAACT GAGAGCTGAG 240
GCTGGAGAGG TAGCGCTCGC CCTAACCTGA TCCTGCAGGT CTCAGGCCCT GGGGTCATAT 300
ACTGCCCCCA TGAAGACAGG GAACCTGTGC TGCTGGTCCC AGAGCACGAA GAGGAAGGGC 360
TGCTGCACCT CAAAGACCAG CAGGCTGCGG GCCACAGAGA TGGCGGAGGC TGCAGCCGCC 420
TCCACCCGAG TCTCTGTGAG TTCCAGCACT GTCTGGTGCT GCATCGCAGA AACCTGAAGA 480
TCTGGGTCTT CTGTGAGCCC ACACAGGTTA AGGTCATAAG AAAAATCGAA GAATTCGAAT 540
TTCTCCATGA TTGAGAGCAT ATCCTGGCTG GTCGTCACCT TGATGCGGGG TAGTGTTAGG 600
AGAGTGGGCT GGAACCTGGA CATCTCCAGT TTCTCCATGA TGGCCTTGAA AACAGAAGGG 660
CTGAGAGCCT GTTCCATGTC TTCAAGACGA TGTTTCAGGT TCTGGGGTAC CAGGATCACC 720
AAACTCAGAT TGTGGGAGAG CTCGAGCTGC CCCACCTTGG CTTTCAAAGT TTGGTCAATG 780
AAATGGGCCA CAGGGTACTT CTTGCTATTG ATCATGGGCA CTTTTATAAC TGAGTTTTTG 840
AAGTGAAAGG GTTCCATTCT GGTTTTCTTG GGATCAAATG TTGTCTTCCA CTGGGCACTC 900
AGGTAGATAG CATTGAGGAG GACAAGGCGG GTATCGGAGG GCAGACTGTC TAGCAGCCGG 960
CTGATCTTGT TGTGGTGTG CTTGGCCACC CAGGTGTTGA TGAGCTCCAA AGTTGAATAG1020
CAAGAAGTAC CTTGTGGCCC ATTTCAATTGA CCAAACTTTG AAAGCCAAAG TGGGGCAGCT1080
GCAGCTCTCC CACAATCTGA GTTTGGTGTG CCTGCTACCC CAGAACCTGA AACATCGTCT1140
TGAAGACATG GAACAGGCTC TCAGCCCTTC TGTTTTCAAG GCCATCATGG AGAATCTGGA1200

GATGTCCAAG TTCCAGCCCA CTCTCCTAAC ACTACCCCGC ATCAAAGTGA CGACCAGCCA1260
GGATATGCTC TCAATCATGG AGAAATTGGA ATTCTTCGAT TTTTCTTATG ACCTTAACCT1320
GTGTGGGCTG ACAGAGGACC CAGATCTTCA GGTTCCTGCG ATGCAGCACC AGACAGTGCT1380
GGAAGTGACA GAGACTGGGG TGGAGGCGGC TGCAGCCTCC GCCATCTCTG TGGCCCGCAC1440
CCTGCTGGTC TTGAAAGTGC AGCAGCCCTT CTTCTTCGTG CTTCTGGGACC AGCAGCACAA1500
GTTCCCTGTG TTCATGGGGC GAGTATATGA CCCCAGGGCC TGAGACCTGC AGGATCAGGT1560
TAGGGCGGAG GCTACCTCTC CAGCCTCAGC TCTTCAGTGG CAGCCCTGCT GCTGCTTGCC1620
TGAATTTGGC CCTCGCCACC TCCTGCCTCA GGTGTCGCTG ATCCACCAAA AGGGCTCCCT1680
GAGGCTCTGG GGCAAGGGAC CGTGCTTCTA ATTAAGCCCT TCTTCCGAATG GGCCTTGCA1740
GGC

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1743

(2) INFORMATION ON SEQ ID NO. 41:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1183 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

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GCCAATCGAA TCGTCTGGG AGGCTTTTCA CAGGGCGGGG CCCTGTCCCT CTACACGGCC 60
CTCACCTGCC CCCACCTCT GGCTGGCATC GTGGCGTTGA GCTGCTGGCT GCCTCTGCAC 120
CGGGCCCTCC CCCAGGCAGC TAATGGCAGT GCCAAGGACC TGGCCATACT CCAGTGCCAT 180
GGGGAGCTGG ACCCATGGT GCCCGTACGG TTTGGGGCCC TGACGGCTGA GAAGCTCCGG 240
TCTGTTGTCA CACCTGCCAG GGTCCAGTTC AAGACATACC CGGGTGTCTAT GCACAGCTCC 300
TGTCCTCAGG AGATGGCAGC TGTGAAGGAA TTTCTTGAGA AGTGCTGCC TCCTGTCTAA 360
CTAGTCGCTG GCCCAGTGC AGTACCCAG CTATGGGGG ACTCAGCAAG CAAGCGTGGC 420
ACCATCTTGG ATCTAGCCG GTCGAGCCCC TGTCCCCACC CTTCCTGACC TGTCCCTTTT 480
CCACAGGCCT CTGGGGGCGAG GTGGCAAGGC CTGGCCGGGC CTTCCTTCCT GGCCCTTAGC 540
ACCTGGCTCT GTCTGCAGCA GGGGCAGGCT GCTTCTTAT CCATTTCCCT GGAGGCGGGC 600
CCCCTGGGCA GCAGTATTGG AGGGGCTACA GGCAGCTGGA GAAAGGGGCC CAGCCGCTGA 660
CCACTCACT CAGGACCTCA CTCACTAGCC CCGCTTTGGG CCCCTCTCTG TGACCTCAGG 720
GTTTGGCCCA TGGGGCCCTC CCAGGCCCTT GCCCCTACTG ATTCTGCCCA GATAATCGTG 780
TCTCTCGCTT CCACTCAGCT GCTTCTCAGT CATGAATGTG GCCATGGCCC CGGGGTCCCC 840
TTGCTGCTGT GGGCTCCCTG TCCCTGGGCA GGAGTGCTGG TGAGGAGGTG GAGCCTTTTG 900
AGGGGGGCCT TCCTCAGCT GTTCCCCAC ACTGGGGGGC TGGGCCCTCG CTCCCGCTTA 960
CCCTCCTTCC CTGACAGCCT GGAGCCTGTA GGGCTGGACT GAGGTTCAGG TCTCCCCCA1020

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GCTGTCTCAC CCCCACTTG TCCCACTCT AGAGCAGGGA GGCAGTGGGG GAGGAGTGT1080
GTCTCGTCTT CTGCTCTCAT GGGGTTTTG GGTGTTTTT TTGTTGTGTC CTGGATTCGG1140
ATAAAATTAA AGAAATGTCT TCCTCAAAAA AAAAAAAAAA AAA

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1183

(2) INFORMATION ON SEQ ID NO. 42:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 768 base pairs
 (B) TYPE: Nucleic acid
 (C) STRAND: individual
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 (A) ORGANISM: HUMAN
 (C) ORGAN:
- (vii) OTHER ORIGIN:
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

```

GTTTTTTTTT TTAGTCGAGA AAATGGTGG TATTTTCACA TTCATAGTGT TTCTATCCAA 60
TTTTCAGTACC CACATTTAAT GAGGAAAAAA TGTTTACCA ATGAAGGAGG AATTCTTAAA 120
TTAGCTGTAA TGTTAGGTTG GAGAAAATT GGTATTAGG GTATTTTCAA GGTACCATCA 180
AATCAGATTT CTGTTTTTTT GTAAAAAAA ATTTTTTTAA TCAGTATTGT TTTTACAAGT 240
AATATACTTT GAAACTCTTG AACTAATAGT CTCAAAACT CTAGAGGACA GCTGAGAAC 300
ACGTATTTCT ATTGTTCTAA ATAAATACAT GTTTTGAAT AGTTCATCA TGAATTATG 360
ACTATGCTTT CATCAAAAGT GTTAATCCCT CTCAGGGTCT CTGGTGAAGA CCTTCAAGAG 420
TTTGGTTTTT TCTCCCAGGA AATTGGAAGG TAGAATTGTA AATTCATAGA ACTTCTTTTA 480
TAATGGTGTA CCTCAGCAGC TGCTTTTCAA TTTATGCCAA GTCCTTACAG AGTTTATACT 540
TGAATAGTAA ATATGCTCTT TGAGTTTAC AGTGTCTTAA ACTCAATGCA CATTTTTTTT 600
TCTTCTTTTT CCACCCCTTC TTGTTTGTAG TTCATTATAC CTGTCCTATT ACAGAACTGA 660
TTTCTTCTCT GGCTGTACAT GTTGGGGTGC TGGATTTTTT TCCGTGCTT TAGTCTTCGG 720
ATACATGTTT TCTTCTTTAG CTGTGGTGA ATACAGTAAT TTGCATTG 768

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(2) INFORMATION ON SEQ ID NO. 43:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 1029 base pairs
 (B) TYPE: Nucleic acid
 (C) STRAND: individual
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO

- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
(A) ORGANISM: HUMAN
(C) ORGAN:
- (vii) OTHER ORIGIN:
(A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

```

CCCTGCTGTG AAGTCTCGGC AGGTGTTGGT AATGTGTGGA AATGCAGTCA GCAAGTTTGC 60
TGGGGAGTTT GATAAAAGTA TAAACAAAA CAAAAAAGC CTCGGTATAA TTTTGTCCA 120
CGACTTCTTC TGTAGCTTTA CACCAGAAGG AAGGAATGGG CTACAGCAGG TAGTGGAGGA 180
AGAGGGGGGT GAGCAGGTGT ATTAATAATG CTTACGGGTA AGGCCTAAAA GGTCACCCCT 240
CGGCCCCCTC TCCAAAAGAA GGGCATGGGC ACCCCCAGGA GAGGATGGCC CCAAAAACCT 300
TATTTTTATA CATGAGAGTA AATAAACATA TTTTTTTTAC AAAAATAACT TCTGAATTTA 360
TCAGTGTTTT GCCGTAAAAA ATATTCCTCT ATAGTAAATT ATTTATTGGA AGATGACTTT 420
TTTAAAGCTG CCGTTTGCTT TGGCTTGGTT TCATACACTG ATTTATTTTT CTATGCCAGG 480
CAGTAGAGTC TCTCTGCCTC TGAGGAGCAG GCTACCCGCA TCCCCTCAG CCCCTCCCTA 540
CCCCCAAGA TTGATGAAA ATTCCAACCA TGAGGATGGG TGCATCGGGG AAGSGTGAGA 600
AGGAGAGCCT GCCTGCTCAG GGATCCAGGC TCGTAGAGTC ACTCCCTGCC CGTCTCCCAG 660
AGATGCTTCA CCAGACCTTG CCTCTGAGAC CTCGCTCTCT GTTCCAGCAA CCCTGGTTGG 720
GGGGTCAGAG TTGATACACT TTCAGGTTGG GAGTGGACCC ACCCCAGGGC CTGCTGAGGA 780
CAGAGCAGCC AGGCCGTCTT GGCTCACTTT GCAGTTGGCA CTGGGTTGGG GAGGAAGAGA 840
GCTGATGAGT GTGGCTTCCC TGAGCTGGGG TTTCCTGCTT TGTCCAGTTG TGAGCTGTCC 900
TCGGTGTGAT CGAGGCTGTG CCTAGAGAGT GGAGATTTTT GATGAAAGGT GTGCTCGCTC 960
TCTGCGTTCT ATCTTCTCTC TCCTCCTTGT TCCTGCAAAC CACAAGATAA AGGTAGTGGT 1020
GTGCTCGA

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(2) INFORMATION ON SEQ ID NO. 44:

- (i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 736 base pairs
(B) TYPE: Nucleic acid
(C) STRAND: individual
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
(A) ORGANISM: HUMAN
(C) ORGAN:
- (vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

```

ATTCCTGGGT TGAAATATTT TGTAGGGATT GCTTATTATA TTATTTTAGC TGATGAACCT    60
CAGGACAACG GCTACAGACA CACACATACA TACACGCACA CAAATCTCA GCTGTTGAAG    120
AGTGGGCTTG GAATCAGACT TCTGTGTCCA GTAAAAAACT CCTGCACTGA AGTCATTGTG    180
ACTTGAGTAG TTACAGACTG ATTCCAGTGA ACTTGATCTA ATTTCCTTTG ATCTAATGAA    240
TGIGTCTGCT TACCTTGTTT CCTTTTAATT GATAAGCTCC AAGTAGTTGC TAAATTTTGT    300
ACAACTTTAA ATGAGTTTCA TTCACCTTCT TTACTTAATG TTTTAAGTAT AGTACCAATA    360
ATTCATTAA CCTGTTCTCA AGTGGTTTAG CTACCATTCT GCCATTTTTA ATTTTATTT    420
AATTTTATTT GCTTGAGCAC ACTGATCAAC CACTGAACTG CCTTCTTCCA TTGTCCTGCA    480
ATGATATAAG GGTTCATTTT TTGTGTATAT GGCTTTCATA GTTGGGATTT CAGAGCACTG    540
ATACCAGATA TTTTCAGTTT GTTCTCTGGG GGAATTTTCAT TTGCATCTAT GTTTTGTAGT    600
ATCTGTGATA ACTTGTTAAA TATTAAAAAG ATATTTTGCT TCTATTGGAA CATTGTGATA    660
CTGCGAACTA TATTCTGTGA AACAGCTGCA GTCAAAAATA AAACACTGAA AGTTTTCATT    720
TTGCAGTGA AAAAAA

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(2) INFORMATION ON SEQ ID NO. 46:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1159 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

GGACCGTGTG TCGGCCGTGG CGCTGCCCAA GCTGCCCATC TCGCTCACCA ACACCGACCT 60
 CAAGGTGGCC AGCGACACAC AGTTCTACCC TGGCCTCGGG CTGGCCCTGG CCTTCCACGA 120
 CGGCAGCGTC CACATCGTGC ACCGGCTCTC ACTGCAGACC ATGGCCGTCT TCTACAGCTC 180
 CGCGGCCCGG AGGCTGTGTG ATGAGCCGGC CATGAAGCGC CCCCACCCG CGGGCCCCG 240

CGTCCACTTA AAGGCTATGC AGCTATCGTG GACGTCACTG GCCCTGGTGG GGATTGACAG 300
 CCACGGGAAG CTGAGCGTGC TCGCCTCTCT ACCTTCCATG GGCCACCCCG TGGAGGTGGG 360
 GTGGGCGCTG CGGCACCTGC TCTTCTCTGT GGAGTACTGC ATGGTGACCG GCTACGACTG 420
 GTGGGACATC CTGCTGCACG TGCAGCCCAAG TATGGTACAG AGCCTGGTGG AGAAGCTGCA 480
 CGAGGAGTAC ACGCGCCAGA CCGCTGCCCT GCAGCAGGTC CTCTCCACCC GGATCCTGGC 540
 CATGAAGGCC TCGCTCTGCA AGCTGTGCGC CTGCACGGTG ACCCGCGTGT GCGACTACCA 600
 CACCAAGCTC TTCCTCATCG CCATCAGCTC CACCCTGAAG TCGTGTGTGC GCCCCCACTT 660
 TCTCAACAGC CTTGACAAGA GCCCCGGCGA CCGGCTGACC GAGATCTGCA CCAAGATCAC 720
 CGACGTCGAC ATTGACAAGG TCATGATCAA CCTCAAGACG GAGGAATTGT TGCTGGACAT 780
 GAACACACTG CAGGGCGCTG CAGCAGCTCT TGCAGTGGGT GGGCGACTTC GTGCTGTACC 840
 TGCTGGCCAG CCTACCCAAC CAGGGTTCCC TGCTGAGGCC GGGCCACAGC TTTCTGCGGG 900
 TACGGCACCTC GCTGGGCATG CTTCCGGGAAT TGATGGTGGT CATCCGCATC TGGGGCCTTC 960
 TGAAGCCAGC CTGCTGCCC GTGTATACGG CCACCTCGGA TACCCAGGAC AGCATGTCCC1020
 TGCTCTTCCG CTGCTCACC AAGCTCTGGA TCTGTGTGCG CGATGAGGGC CCAGCGAGCG1080
 AGCCGGACGA GGCCTGTGTG GATGAATGCT GCTGCTGCC CAGCCAGCTG CTTATCCCA1140
 CCTGGACTG GCTGCCAGC 1159

(2) INFORMATION ON SEQ ID NO. 47:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 690 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

```

AGAGCGGCCG CCCCTCTTTT TTTCTCTTTC TTTTTTTTTT TTTTGCATA TCAGAAATGC    60
ATTTTAATTT TTATTGAAA ACAACTTAAA TTTTGTAGACA AATGATTTTA GTATATAAAT    120
TTGCTTTTGT TTTTATACAG AATATAAAGA TTCCCTCAT TAATCTTCCA TGTGAAGGGT    180
ATTACAAGCC TGGAGGAAGA TACTTTCTGC ACACAAGTAT GTATCTTATG TGTGCAGTAT    240
TGGAAACCAA TGGGTGTAGT CTCTACACA TAAATGGGGT CAAGTGACAT CACAAATTAA    300
AAGGGGGAAG AGAAATATT CTAGTTAATC AGATGCAAGA AGCAACAAG ACGCAAAAC    360
TGTGCAAATA AGACCAAGCC AGTAACTTA GTTACGACAC TGCAGATTAC ACTGGAATAA    420
CAGGTTTGTG AGGCTATAGT GTGCACCACA TTAACACAGC AAGAAGAGC TATTTATATA    480
GAAAGGCTGG AATGAGGGAT TTTTACTAAA GCAAATTAAC TTCTTGTCAG CTGCCAAAC    540
AAAACAAAC TGAGCATATG AGTGTTAGTA TACTGAAGGC ATGTTATACC AGTTTCTGTG    600
CAGCATGCTA AAAGTTAGAA CTTCTTCACT GGTGCTTATC AATCATTAAT AGTCACGTTT    660
TTGCCCTTC TTGCCAAATT TCGAGGCATG

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690

(2) INFORMATION ON SEQ ID NO. 51:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1186 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

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ACCATAGATT TATTTTAAAA GGGAAAAATCT CACACATAAT TAAGCAGTGG AAAATGTGCT 60
CAATGCTATG GTGCGTCAGG CCCTCTGTCT ACCAGGTTTC TCCCGCTTTC TGCAGAGCTG 120
TGGACCCCTGT ACGTACCAAA CAGGTGAAC TGGTCCATCT TTCCTTCTTC CTTTTTTTGC 180
ACATTTGTCAT TTATATCTTC CTGTACTAAA AGAAACAAAT TATTTATAAT TGGGGTGACA 240
ATATAAAGGA ACAAAGATG GGGCAATAGT TGCTTCCTAG CTGGAGCTGT AAGTCCATGT 300
TACAGAAACT CACTATTTAA AAAGTTTTAA AGATTTATG AACCTTGTC TACAATTCGC 360
TGAATACTTA TTTGTCTTTT AAACCTCCCT CGGTGTATGG ATCATCTTCG TCAGAATGCC 420
GTTGTTTCAT TGTGAATCAG GGGAAAATGT TAATCATTG GAGACTGTTT TCTTATTACC 480
AAATGTACAA TCCATAAGAC AACTGAAAGC AACAACTGCT GGGTTCACGT ACAAAGATTA 540
TAAAAATCAT CACGTTCAAA GTAGAGTTTT TAGCCAAGGT CAAGAATAA CCTGGGGCTG 600
AGTCAGCGTC TCTACCCACT TAAATAACAG CGTAAAGATC TTTCACTAAA TTCGTTATGT 660
GGTCTGCTG GATGTAAACC TATATATTTC CTTTGAAC AGAATCATAT CTGCAGACT 720
CTTGGCACTC CTGCTAGCT TTGACCGAAT GTTCACTCTC ATCGTAATGG AAGATTCTTA 780
TCTATGCAGA TAATACATGT TTTTAAATAC TGTTTCTGT TTAGTCTCTA ATCTTCCTAA 840
CTCAAATTGG GGACTGAGGA GAGAGAAAG TGTTTACCCC TGTTACCGTG CCATATTCTT 900
CTTGCTGCTT TTCAACCCCA CGTGATTGTT GATTGACGGT TCTGCTATAA TGTGCGTGCC 960
CTTCAAGTTT CAGAAAACCT TCCCAATCAT TTCACTTCAA TCTTAATTGA ACCCAAGAGT1020
CAAAGTTATT ATTTTCTCCG AACGTGTTG TGATCTTCTG TTATATTTTG GGGCATGTTA1080
CCTTTATGGT ATATAAGCTG TAGTGCATAC TCTTTGTATT GCAAAAAACT GTTCAGTAAT1140
TTATGTACAT GTATTCCACA TTTTAGTGTG CTGAAGTGA CAATCC 1186

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(2) INFORMATION ON SEQ ID NO. 52:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1029 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

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GGGAGAAGGA GGAGGCCGGG GGAAGGAGGA GACAGGAGGA GGAGGGACCA CGGGGTGGAG 60
GGGAGATAGA CCCAGCCCAG AGCTCTGAGT GGTTCCTGTG TGCCTGTCTC TAAACCCCTC 120
CACATTCCCG CGGTCCCTCA GACTGCCCCG AGAGCGCGCT CTGCCTGCCG CCTGCCTGCC 180
TGCCACTGAG GGTTCCCAGC ACCATGAGGG CCTGGATCTT CTTTCTCCTT TGCCTGGCCG 240
GGAGGGCCTT GGCAGCCCCT CAGCAAGAAG CCCTGCCTGA TGAGACAGAG GTGGTGGAAG 300
AAACTGTGGC AGAGGTGACT GAGGTATCTG TGGGAGCTAA TCCTGTCCAG GTGGAAGTAG 360
GAGAATTTGA TGATGGTGCA GAGGAAACCG AAGAGGAGGT GGTGGCGGAA AATCCCTGCC 420
AGAACCACCA CTGCAAAACAC GGCAAGGTGT GCGAGCTGGA TGAGAACAAAC ACCCCCATGT 480
GCGTGTGCCA GGACCCCAACC AGCTGCCCAAG CCCCATTGG CGAGTTTGAG AAGGTGTGCA 540
GCAATGACAA CAAGACCTTC GACTCTTCTT GCCACTTCTT TGCCACAAAG TGCACCCTGG 600
AGGGCACCAA GAAGGGCCAC AAGCTCCACC TGGACTACAT CGGGCCTTGC AAATACATCC 660
CCCTTTCCTT GGACTCTGAG CTGACCGAAT TCCCCTTGGC CATGCGGGAC TGGCTCAAGA 720
ACGTCTGGT CACCCTGTAT GAGAGGGATG AGGACAACAA CTTTCTGACT GAGNAAGCAG 780
AAGCTGCGGG TGAAGAAGAT CCATGAGAAT GAGAAGCGCC TGGAGGCAGG AGACCACCCC 840
GTGGAGCTGC TGGCCCGGGA CTTGAGAAAG AACTATAACA TGTACATCTT CCCTGTACAC 900
TGGCAGTTGC GCCAGCTGGA CCAGCACCCC ATTGACGGGT ACCTCTCCCA CACCGAGCTG 960
GCTCCACTGC GTGCTCCCTT CATCCCCTAG GAGCATTGCA CCACCGGTT TTTCGAGACCT 1020
GTGACCTGG

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(2) INFORMATION ON SEQ ID NO. 53:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 985 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

ATCACTCTTT	CTCAGCTCGA	CTGGAGTTTC	TGCACCTTTG	CAGGGGGCAA	GTAAGTCCCT	60
GCACCCTGAA	CCACCCCCCA	TTCTTGTTCA	TTTCAGCAGA	TAATGATGGA	GGGGGGGGGG	120
TGTCCATCGT	GCTGAGGGTG	TGACCGCAAG	AGGGTGAAAA	CTTCCAGCCA	ACTTCTCAG	180
TCCTTCTCT	TGCGAGAGGG	AAGCCACCTG	CTATACAAAC	TAATACCCCC	TGCCTTGACC	240
CCTTCCCCAC	GACTCAGTTG	ACAGAAGGAT	ATACTTGTT	ATAACTTATT	ATTTTGTTCT	300
CTGTAATAC	AAGATGTTTA	TAGGAAATAT	GTATTCTGAA	CTCTATCTGC	AGAATGAGTC	360
ACTACACCAA	AATAGTTCTA	TTATTTAGAA	TGTGTTAATT	TTAAAGGGAC	CTGATAGCTA	420
TTTATTTACA	TATGCGATCC	ACATTGTGT	GAAAGCATGT	GATCATACTA	ACCCAGCCTC	480
CTGGAATGTC	GCTGTACGAT	GATTGATGTC	TTTTTCTCAG	TCCATAGTTA	CAATTGTTTA	540
GTATGCTAAT	CAGTCCAGTT	CCCTGAGGTT	TAAGATCAAA	TATAAATTAC	TCTGCTTTTC	600
GACTCATTTA	GGTAGCATTG	TACCTGAACC	TGATTGCTAC	TTTTTCATCT	TAAATATTAT	660
ATTTCTCAT	CTAATCTGCC	TTCCCCTCAT	CCACAGACAT	TTGGAGAAGG	AAATGGGAGG	720
GTGCTGTTA	TCCCTTTCTC	TTTGCTTTGT	CCCCGTTGTT	AGACTGGCAG	CGTCAGTTGC	780
TCGGTGGGCT	TGGTTAGAGC	CGTGGGTGAG	GCAGGTGGCT	GGCGGGGACA	GGGAGAGGCT	840
GAGAGGGAAG	TGGTGGCATT	TACTGCTCTG	ACACTTCCAC	TGTCCCTGCT	GGGGATGCTG	900
GGGCCAAGGC	CTGTGGGGCC	TGTGAACTGC	ACAGCCAGGA	GCAAGGAACC	CACTAAATAC	960
TCCGTCAC TG	CATGTCCCCT	CTACA				985

(2) INFORMATION ON SEQ ID NO. 54:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 622 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

ATGTTTTTCA	TTTTTTTCAT	GTTATCTATC	CAAGCACTGT	TCCATGGTCA	GCAAGTCATA	60
TTTCATAATG	TGGATTTTCC	AAAAATAATTA	TTGAATACAG	CTATTCTATG	GCTACTTTTA	120
GTGTTTTTGT	GGTATGTGGT	GIGGGAGTGT	TTATGGAATT	ACCAGTATCT	TAAATTTTCA	180
AAGGAACCTT	GGAAGTCTAT	CACTCTAAAT	GAAAGTCTGT	CACTCTACAT	GAATTATGTG	240
CTCAAATTTG	ACCAACTCAG	TTTAAGACAC	AAAACAGTAA	TTTGAAGAAG	GAAAAATGAA	300
GAGAGTTTCT	AGTTTAATGG	GTTAAATTTT	TGTTGTTGCA	ATAGTAAGTT	TAGCTTTCTT	360
ATAATATTTT	TAAATGAAAA	ATCATAGGTA	TTTGTTACCA	TGTGTGAAGA	TTACTTTGTT	420
AAAAGCAAAA	GTGGTCGTGT	GATATGCTAA	ATGTTAATTA	CTGATTTTAT	ATGTTTAAAT	480
CACGCCAAAC	AAATTATGTC	TGTGCCATCC	AGGGTCTGTT	GTTAATCTTT	TTCTGAGTAC	540
TTGGATTGGG	ATAAAGGGCT	TGTACTATGC	ACTTTTATT	AATGAATAAA	TAGAAAACGT	600
TAGTAACAAA	AAAAAAAAAA	AN				622

(2) INFORMATION ON SEQ ID NO. 55:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1129 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

```

GATTTTTATC TAGAAACTAT ATTACTTAA ACCCCCCTCA GGAAAGAGGT TTAAAAATCA 60
AAGATGGGAA AATCGGAGAA AATTGCCCTT CCCCATGGCC AGCTTGTTCa TGGTATACAC 120
TTGTATGAGC AACCAAGAT AAACAGACAG AAAAGCAAAAT ATAACCTGCC ACTAACCAAG 180
ATCACCTCTG CAAAAAGAAA TGAAAAACAAC TTTTGGCAGS ATTCTGTTTC ATCTGACAGA 240
ATTGAGAAGC AGGAAAAAAA GCCTTTTAAA AATACCGAGA ACATTAAAAA TTCGCATTTG 300
AAGAAATCAG CATTCTAAC TGAAGTGAGC CAAAAGGAAA ATTATGCTGG GGCAAAGTTT 360
AGTGATCCAC CTCTCCTAG TGTCTCTCCA AAGCCTCCTA GTCACCTGGAT GGGAAAGCACT 420
GTTGAAAAAT CCACCAAAAA CAGGGAGCTG ATGGCAGTAC ACTTAAAAAC GCTCCTCAAA 480
GTTCAAACTT AGATTTCAGA TTTCAGTATG TGTGTAATAA ATAATTTTTC CCATATCCCT 540
GGACTCTTGA GAAATTTGGT ACAGAAATGG AAATTTGCCT TGTTGCAACA TACAATTGCA 600
AAAGATGAGT TTAAAAAATT ACATACAAAC AGCTTGTATT ATATTTTATA TTTTGTAAT 660

ACTGTATACC ATGTATTATG TGTATATTGT TCATACTTGA GAGGTATATT ATAGTTTGT 720
TATGAAAGTA TGTATTTTGC CCTGCCACa ATGCAGGTGT TTTGTATATA TACAATGGAT 780
AAATTTTAAG TGTGTGCTAA GGCACATGGA AGACCGATT TATTGTCACA AGGTACTGAG 840
ATTTTTCCTA AGAACAGCT GTCAAAATCTC AAGGTGAAGA TCTAAATGTG AACAGTTTAC 900
TAATGCACTA CTGAAGTTTA AATCTGTGGC ACAATCAATG TAAGCATGGG GTTTGTCTCT 960
CTAAATTGAT TTGTAATCTG AAATTACTGA ACAACTCCTA TCCCCATTTT TGCTAAACTC 1020
TAATTTCTGGT TTTGGTATAT ATCCATTCCA GCTTAATGCC TCTAATTTTAT ATGCCAACAA 1080
TAATTTGTTGT AATCAATTTT TAAAAATAA ATAATTGGGG CCCCCCTT 1129

```

(2) INFORMATION ON SEQ ID NO. 58:

- (i) SEQUENCE CHARACTERISTIC:
- (A) LENGTH: 877 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

- (iii) HYPOTHETICAL: NO

- (iii) ANTI-SENSE: NO

- (vi) ORIGIN:
- (A) ORGANISM: HUMAN
 - (C) ORGAN:

- (vii) OTHER ORIGIN:
- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

CACACTGAGG	TTTTTAACA	CCATTCTCCC	CCACTTCTCT	CCTGGGTGAC	ATAAGAGAGA	60
AATAACCTGT	AGTACAGCAG	CTAAAGTATT	CTCCTTTCAG	AGAATTTTTT	TGGAGGTCTC	120
TAATATATAT	TTCCCCCTTG	TCTCTGTGAT	CTCTTATTTA	TACTATATTA	TGTGCCCATG	180
TACTTTCTAA	ACTGAGCTTG	GAACATTTAG	TATTCTTGCA	ATTGGACTTC	CCACTTAACA	240
ATTATACAGA	CTTTGCTTTT	AGAAATAGAT	TAGGTTCCAA	ACAGAAAGTT	CAAGTGTAAC	300
AACAACAATA	AAAATAGATT	ATGAAACAGG	CTATAATGG	CTCTTTTGGG	JTTGATAGGG	360
GCAAGATGAA	AGGCAACTTT	CTTGCTTTTG	AAATCATGTT	GGGTAAGAGG	TAAGGAATCC	420
AGCTACAATT	TTATTAGTGC	TGAAACGGG	CTTCCTTGAA	TTCTCCAGGC	CCTATCATT	480
TTTTTTTTCT	TACTAATCAG	AAGAGAGCTG	GGGTAGAAGC	CCCATGTTTG	TATTCCATGA	540
AACACGTCGG	GTTGGAGTAA	AGGCAAAAAC	AGCTAGACAC	ACCAGGTGTG	TCTGTTTGAC	600
ATTTATAAGC	TGGCACTCAT	CAACACTCCT	GTTTCTCCTT	TCTCTGGGAC	GTGTGGATTA	660
AGGGGTGTGA	GTTGTGGGAA	GAATTGCCCT	CGTACCTCCT	GGATTATTA	TTTTTCTCAA	720
ATACCAACCA	GTAAGATCCC	AAATAACTTG	AGAAAAATTG	TTTCTGTATC	TGTCCACTTC	780
TGGTGTCAAA	GATTTTACTC	ATCTTCTTAG	TACATTCTAT	GTATTTTATA	TGTATAATTT	840
TATACAATTA	AAAATAGATT	TTGTCTAGT	GAAAAAA			877

(2) INFORMATION ON SEQ ID NO. 59:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1329 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

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GTCGGGGAGC GCGGGGCGCG GGGCCAGGGG ACCCGGGGCC ACGGAGAGCG GGAAGAGGAT 60
GGATTGCCCG GCCCTCCCCC CCGGATGGAA GAAGGAGGAA GTGATCCGAA AATCTGGGCT 120
AAGTGTCTGGC AAGAGCGGATG TCTACTACTT CAGTCCAAGT GGTAAGAAAT TCAGAAGCAA 180
GCCTCAGTTG GCAAGGTACC TGGGAAATAC TGTGATCTC AGCAGTTTTG ACTTCAGAAC 240
TGGAAAGATG ATGCCTAGTA AATTACAGAA GAACAAACAG AGACTGCGAA ACGATCCTCT 300
CAATCAAAAT AAGGGTAAAC CAGACTTGAA TACAACATG CCAATTAGAC AAACAGCATC 360
AATTTTCAAA CAACCGGTAA CCAAAGTCAC AATCATCCT AGTAATAAAG TGAATCAGA 420
CCCACAACGA ATGAATGAAC AGCCACGTCA GCTTTTCTGG GAGAAGAGGC TACAAGGACT 480
TAGTGCATCA GATGTAACAG AACAAATTAT AAAAACCATG GAACTACCCA AAGGTCTTCA 540
AGGAGTTGGT CCAGGTAGCA ATGATGAGAC CCTTTTATCT GCTGTTGCCA GTGCTTTGCA 600
CACAAAGCTCT GCGCCAATCA CAGGGCAAGT CTCCGCTGCT GTGGAAAAGA ACCCTGCTGT 660
TTGGCTTAAC ACATCTCAAC CCCTCTGCAA AGCTTTTATT GTCACAGATG AAGACATCAG 720
GAAACAGGAA GAGCGAGATG AGCAAGTACG CAAGAAATTG GAAGAAGCAC TGATGGCAGA 780
CATCTTGTGCG CGAGCTGCTG ATACAGAAGA GATGGATATT GAAATGGACA GTGGAGATGA 840
AGCCTAAGAA TATGATCAGG TAACTTTCGA CCGACTTTCC CCAAGAGAAA ATTCCTAGAA 900
ATTGAACAAA AATGTTTCCA CTGGCTTTTG CCTGTAAGAA AAAAAATGTA CCCGAGCACA 960
TAGAGCTTTT TAATAGCACT AACCAATGCC TTTTATAGTG TATTTTIGAT GTATATATCT1020
TATTATTCAAA AAATCATGTT TATTTTGAGT CCTAGGACTT AAAATTAGTC TTTTGTAAATA1080
TCAAGCAGGA CCCTAAGATG AAGCTGAGCT TTTGATGCCA GGTGCAATCT ACTGGAAATG1140
TAGCACTTAC GTAAAAGATT TGTTTCCCCC ACAGTTTAA TAAGAACAGA TCAGGAATTC1200
TAAATAAAT TCCAGTTAA AGATTATTGT GACTTCACTG TATATAACA TATTTTATA1260
CTTTATTGAA AGGGACACC TGTACATTCT TCCATCATCA CTGTAAGAC AAATAAATGA1320
TTATATTCA
1329

```

(2) INFORMATION ON SEQ ID NO. 60:

- (i) SEQUENCE CHARACTERISTIC:
- (A) LENGTH: 697 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

GTAGGCCTA	GTCTGGCGC	AGAGSTTCT	GGGAGCCAAG	AGTGGAATG	GCGTCTGTAT	60
GATCTTCGGA	GCCTGCTGCA	TCGGACCTCG	GCCAGTCATA	AAAGATGACA	ACAGCAGCCA	120
GGCCAACTT	TGAACCTGCC	AGAGGTGGAA	GGGGAAAAGG	AGAAGGIGAT	TTGAGCCAAC	180
TTTCAAAGCA	GTATTCAAGC	AGAGACCTAC	CCTCTCATAC	AAAGATAAAA	TACAGACAGA	240
CTACTCAGGA	TGCCCTTGAA	GAGGTTCTGT	ACCGTGACTT	CAGGAGAGAG	TTGGAAGAAA	300
GAGAGAGAGC	TGCTGCAAGA	GAGAAAAATA	GGGATCGTCC	AACCCGAGAA	CATACAACCT	360
CCTCTTCAGT	GTCAAAAAAG	CCACGGTTAG	ACCAGATTCC	TGCCGCCAAC	CTTGATGCAG	420
ATGACCCCTCT	AACAGATGAG	GAAGATGAAG	ATTTTGAAGA	AGAAAGTGAT	GATGATGATA	480
CTGCAGCTCT	TCTTGCAAG	CTGGAAAAAA	TTAAAAAAGA	AAGAGCTGAA	AAGGGCCAAG	540
GCCCAGGGAA	GGGACCAAGG	GCCAAAAAAG	CTTTAAGGGG	GGGAAGGGTT	TCGTTTTGGG	600
AAAACATTGG	TTGGGCGGGA	AACCCCTTCC	CTTTAATCTT	GAGCTTGGCC	CATTCCAAGC	660
TTAAGGCCGA	CTTTGAAAAG	TTTGAAAGGA	GGGTGGG			697

(2) INFORMATION ON SEQ ID NO. 61:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1389 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

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CGAAGAATAG AATTGGCCAG GACCTAGGTT CTCATATTCT TGGTATTCTT CCTGGATGGA 60
AAGGCTGTGG GCATCAATAG GGGACAGAGG CTGATGCTGG AGTGGCCAGT AGAGGTGGTG 120
GAGCAGAGCA GCCATCTTTT AAGTGGGGCT GTATCAGGCT GGGTTTATTT AAAAGCAACA 180
AAATGTTTTG GTTAAGAAAAA TTATTTTGTCT TTCAGTGTA AATCTTCGCAG TGTCTCTAAC 240
AAAGTTCAGT CTCTGTGCTG CCCCTTTCCC TCACCTGATGT CTGCACTTGG TTGAGGTCTC 300
CTGGAGCCTC ACAGGCTCTG CTGTTCTCCA CTCTCACCT GCCATCCACG CCTGCAAGC 360
TCATGCAAAAC ACCCTTTCTT CCTCTGCGG CAGAGTTGTT CAGGTTGCCT GGGCAGGGGC 420
TTAAACAGTG CCAGCCCCCTG CCATCCCAAA GCTATTGTTA AGCCCCCAGC GCGTCTCTCA 480
CCCACGCCCA CTAGCCTGCC ATGTCCACAG TTCCTTGGGC TGCTAGGGGG CTAGTGCACT 540
GGTCCTGACC TCTCTTATCA AGAGCACACT TCTTTGCTGG TTGCTCCTTT TGAGCATATG 600
CGTGTGATTA TTTGGAACAG TTAGACTTGC CACGTTGGGT CAGTTTTAGA AATGTGTTCT 660
AGCTAGAGGG ACTGGTGTCC TTCCAAGTCT AGCATTGGG GTATGGAAAA TTGTGTGGT 720
GTGTGGTAGG GTTTTGTGTT TCTTTTTTGA GTTTTTTTC CCCCTTTAGT TCCTGGCTT 780
TTTCTTTTCC CTTCCTTCTT CCACTGGCCN AGCTTGGGCC TCATCTCAT GTCATCTTCT 840
TAGGAAGGGC CTTGCCCCAT CTGTCTGCC GGCAGCATGC ATCCAAGGCC AGAGCTCAGG 900
CCTGCAGACT GGGCTGTGTC CTCTCCGCT TCAGGGTATG GGAGTTGGTG AAGGGGCTTT 960
CAAAAAATAA TAAGAAAAAA AAGGTAAGT CTTTGTAGC TTCTATCCAC TCAGATCTCTG1020
GAAGGCAGCA AGGTTTTGTG GATCTAGATT CATTAGGAAT GTCTCTCTGT CAGCCAGGCC1080
AGGACCCGGG CTGCGCAAGA GCAGAGGCC TCACAGCAAC CAGGATACCA CCACCTTTGGG1140
GGCTTTGTGT ACAGAGGTCC GGGTCTGAGA CCTCATAGGC TGCAGAAATC TGGGGCAGCC1200
ACCATCAAGA AGCCCCTCTC AGGGGCCAGA ACTCCTTTCG CAGCGTGGAT TTCTCAAGTC1260
GGGACTGCAT AATTAAAGCA GTTGCAGTTT TATTTTTTTT ACAGCTTTTT TCCCAAAAAT1320
GATTTGTAGT TGTGTGTGCA GCACTTCGCC CTGATATGTG TGCTCTACAA TAAAAACCA1380
ATCTAATAT

```

(2) INFORMATION ON SEQ ID NO. 62:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 535 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62:

TGTATTGAGG	TAATAAATTG	TTTACTGAC	AATTTTCCT	TTTTCTACAC	TAAAAAATA	60
TGTGATATAT	TTCCCTCTT	GAAGAGGCAA	TCATTAAAC	TCTCAAATTT	TCTATAGAAT	120
CAAGATAGAA	CCTTTAGATA	CTCCAACTCA	CCAAAATGTA	AAAAAACTAA	CAAAAATATT	180
TGGTCTTCAA	TAATGCTAAA	TATCTACATT	TTTAGAATTT	ATCAACATTT	AACTAGATAA	240
TTGGGCATGT	CTTAATTATG	CATGTACTTA	TCCATACTAA	TAAAATTGAC	AATGCTAGTG	300
CATACTTATT	GGTTTAGTCC	TATTATCAGG	ATATAATCAT	CTGTGAGGAG	GATATTTTAA	360
ATACTGTAAA	TGATAACAGT	TAATGATATA	CACATTTAGA	CTGAGTTGCA	CACTGGCAGG	420
GAGACCAAAA	ACATTACTTC	CATACTTGTC	TCATGATTCT	TTTTTTTTTG	AGAGAGTCTC	480
ACTCTGTCCG	CAGGCTGGGA	GTACAGTGGC	ATGATCTCGG	CTCACTGCAA	CCTCT	535

(2) INFORMATION ON SEQ ID NO. 63:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1098 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

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GTGATTTGAC ATTTGAACAA ATTAGGAAGC TGAATCCTGC AGCAAACCAC AGACTCAGGA 60
ATGATTTCCC TGATGAAAAG ATCCCTACCC TAAGGGAAGC TGTTGCAGAG TGCCTAAACC 120
ATAACCTCAC AATCTTCTTT GATGTCAAAG GCCATGCACA CAAGGCTACT GAGGCTCTAA 180
AGAAAATGTA TATGGAATTT CCTCAACTGT ATAATAATAG TGTGGTCTGT TCTTTCTTGC 240
CAGAAGTTAT CTACAAGATG AGACAAACAG ATCGGGATGT AATAACAGCA TTAACTCACA 300
GACCTTGGAG CCTAAGCCAT ACAGGAGATG GGAACCACG CTATGATACT TTCTGGAAAC 360
ATTTTATATT TGTATGATG GACATTTTGC TCGATTGGAG CATGCATAAT ATCTTGTGGT 420
ACCTGTGTGG AATTTCAGCT TTCCTCATGC AAAAGGATTT TGTATCCCCG GCCTACTTGA 480
AGAAGTGGTC AGCTAAAGGA ATCCAGGTG TTGGTTGGAC TGTTAATACC TTTGATGAAA 540
AGAGTTACTA CGAATCCCAT CTTGGTTCCA GCTATATCAC TGACAGCATG GTAGAAGACT 600
GCGAACCTCA CTTCTAGACT TTCACGGTGG GACGAAACGG GTTCAGAAAC TGCCAGGGGC 660
CTCATACAGG GATATCAAAA TACCCTTGT GCTAGCCCAG GCCCTGGGGA ATCAGGTGAC 720
TCACACAAAT GCAATAGTTG GTCACTGCAT TTTTACCTGA ACCAAAGCTA AACCCGGTGT 780
TGCCACCATG CACCATGGCA TGCCAGAGTT CAACACTGTT GCTCTTGAAA ATCTGGGTCT 840
GAAAAAACGC ACAAGAGCCC CTGCCCTGCC CTAGCTGAGG CACACAGGGA GACCCAGTGA 900
GGATAAGCAC AGATTGAATT GTACAATTG CAGATGCAGA TGTAATGCA TGGGACATGC 960

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ATGATAACTC AGAGTTGACA TTTTAAACT TGCCACACTT ATTTCAAATA TTTGTACTCA1020
GCTATGTTAA CATGTACTGT AGACATCAAA CTTGTGGCCA TACTAATAAA ATTAATAAAA1080
GGAGCACTAA AGGAAAAA
1098

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(2) INFORMATION ON SEQ ID NO. 64:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1860 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64:

TAAGATCCTG	ACTCTGAAGC	TTCAAAGTGA	CACTGTGGAA	ATCTGAAACG	AGGGGATGTC	60
ATGAAGGCAG	CTTTTCTTTT	TCTGAGGAAA	AAATAGGCAT	GGGCTACAGG	ACTATTTAAA	120
ATGTCTCATT	TACAGTATAA	AACTCAAAGG	TAGATGTAAT	TTTACACCT	ATGAGTATTT	180
GTCCAATTTT	TGCTCTTTCC	TCACCATTTG	GTATCTATTC	TTTATATGTA	AATAAGATAA	240
GGTCATCTGA	TAGCCTTATT	CAGTCTTCAT	CATTTTCATC	ATTGTTCCTA	TGTAGATTAT	300
TGGACATTTA	TGTAGCACT	ACATAACTGA	TTATAAAAA	CTGTAATGTA	ATTAGCACTT	360
TCATATTGAA	ACAAGCCTGC	TAGCCTATGT	ATAAAATAGC	AAAATGTTTG	CTGTTTATAA	420
AAAGATGTAA	TGGGGTGGGG	GGCAGGGGTA	ATTTCAAGTT	ATTAATTTAA	AAATGAACATA	480
GCAATTTTGT	ACCTGGTGAC	TTTGTGGTGC	ACTCACCTCT	GATAGTGAAT	TGAATTCGGT	540
ATGTAAAAAG	GGGTTAGTGG	TATTTTCATTG	CTGCTAAAAA	TGACAACTCC	CTCTGTGTCC	600
TGTTTTTCTT	AAAGCTGTCA	GTGTACAAGT	GGGTATTTGA	ATACCAGACC	TTACTGTAAA	660
AAATAAAAAA	GGTGGTATCT	AGAGCATGTA	AATGGATAT	AAAGTTCTGC	TCTTAAAGAG	720
TTGATCTAAG	AGTATGGCTA	AACATCTATA	TATGCAATCT	ATTAAGAGAA	CTTAATTCGG	780
CTATTATGTC	TTGATTGTAT	TGCAGTTTTT	TCCTAATTAT	AACAAATTTT	TCCTCATTTG	840
CCTGTTTTTA	ATCCTGTGCC	TAGAAGGAGT	ACAAAATGCA	CACTTTACAA	AATTGATATT	900
TAACACTTAC	CCACTCCCCCT	TTCCCCATCT	CTTCTACCGC	TCTTGTTGAT	CGTGGTATCT	960
GATCTTGAAT	AGATAGGCTG	AAGGCACATG	GTTCCCTCCA	AAAACCACTA	TTGATACCAC	1020
TACAAAAACA	AGCCAGCAAA	AAGATACTGT	AGAGAGGTTG	GCTTGCTTCC	CTCTCTTCCT	1080
AACATGCATG	TGAAAAATAA	GCCGTTATTG	ATCTTAAACA	TGGGTCAGAT	GAGTCATACA	1140
TTGGGTTATT	TTTTATATAC	ATGTATACAC	AAAATATTTT	AAATTTGAAAG	CAACATCTTA	1200
ATGGATTCAA	AACTATTACA	AGCTGTTGTC	TAAACAGGTT	GAGAAAAAAA	TTTATAACTG	1260
TAAAAACAAA	TGCACATATT	GATATTTAAA	ATGCGTAATT	AAGAAAAACC	ATTGTTGTTG	1320
TGTTTTTCTT	GTATACCAAT	AATTAAGCCA	CTACTGTTGG	CACTGTTTGG	TTTTCTATTT	1380
TAACACTGAA	GGAGTGAAAG	TATTTCCCTAT	ATTTATGAAT	TTACTACTAA	AATCTTGCCA	1440
AAAAAAGAAA	AAAATTGTCT	AACGTGTGTG	GGTGAAACT	GTTAATCAAG	TGTTTCTACT	1500
CCCCCCCCGAA	AATCCCCCTGA	AAGTTGGACA	CCAAGTGTAT	ACCTAGGTTT	GCTTAAAGGG	1560
ATTTCACTAT	TATATAAAGT	CAATAAAAAA	GAAGTAGTTG	TATATATGCA	ACATTGTGTA	1620
CAGAGGGGAA	ATAATGAATA	GTATTAAGA	AACATTCTCG	TCTTCCTTTA	CCTTTAATCC	1680
CCTAATACCT	AGTCTACTTT	TTAAATTTTC	AGACTTCACT	GCTTTTGAAA	TTGATAATTCT	1740
TAATTTTCAC	ATTATTGTTA	ATGGAATAAT	ATATCTAATA	AAGTTTTTAG	TTATTGCCAT	1800
GCCAGATATG	AAAATTCTCA	TTTGCTGAGG	TTTTGTTTCA	AGAAAATGTA	TTGGCATGTC	1860

(2) INFORMATION ON SEQ ID NO. 66:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 205 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66:

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CRTWSILRGR MWLSTNSAAD AINPWPGRSS RPRSRAAVPH RLLHLPPVCA ELQGQQFYSL 60
EGAPYCEGCVY TDTLEKCNIC GEPITDRMLR ATGKAYHPC FTCVVCARPL EGTSFIVDQA 120
NRPHCVPDYH KQYAPRC SVC SEPIMPEPGR DETVRVVALD KNFHMCKYKC EDCGKPLSIE 180
ADDNGCFPLD GHVLCRKCHT ARAQT 205

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(2) INFORMATION ON SEQ ID NO. 67:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 150 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

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AARALKRFPF SGPPLRDRSP SLESQSRKTP RLPEDLASGK KDYTFQRPLR RRDRKRRASR 60

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VSLRVDPDSH GPGGVVADEV PHQKCGWGR RLPGVPRGAA GAQRQEPGSP TEGWGGGPPR120
HVPVQPVRVS ADRPADTAP SPSKDLLSHF 150

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(2) INFORMATION ON SEQ ID NO. 68:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 55 amino acids
 - (B) TYPE: Protein

- (C) STRAND: individual
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68:

LLECRHHDGD VSSVGGPLQG PRVLQGGLGV CEGAHQVASQ QGRLPRPERA GLPLT 55

(2) INFORMATION ON SEQ ID NO. 69:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 182 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

SVHFPAALRC ETAALLWSLR AARHDSQRT LRRARKTTPS RGLCGAATGS GGRAECPCAW 60
 IRATMVARVW SLMRFLIKGS VAGGAVYLVY DQELLGFS DK SQAALQKAGE VVPPAMYQFS120
 QYVCQQTGLQ IPQLPAPPKI YFPIRD SWNA GIMTVMSALS VAPSKAREYS KEGWEYVKAR180
 TK 182

(2) INFORMATION ON SEQ ID NO. 70:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 25 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70:

PEDSGLGPHS EGRPPDCRPN KGLQK

25

(2) INFORMATION ON SEQ ID NO. 71:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 56 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71:

DEKNTSFLYS DVGATSMKSV LYESTYKMR HLVNCARYLK CMFRKAFYQL RNMTYF 56

(2) INFORMATION ON SEQ ID NO. 73:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 291 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73:

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LERLVDIKKG NTLLOLHLKR IISDLCKLYN LPQHPDVEML DQPLPAEQCT QEDVSSSEDED 60
EEMPEDTEDL DHYEMKEEEP AEGKKSSEDDG IGKENLAILE KIKKNQRQDY LNGAVSGSVQ120
ATDRMLKELR DIYRSQSFKG GNYAVELVND SLYDWNVKLL KVDQDSALHN DLQILKEKEG180
ADFIILNFSF KDNFPFDPFP VRVVSPLVSG GYVLGGGAIC MELLTKQGSW SAYSIESVIM240
QISATLVKKG ARVQFGANKS QYSLTRAQQS YKSLVQIHEK NGWYTPPKED G 291

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(2) INFORMATION ON SEQ ID NO. 74:

- (i) SEQUENCE CHARACTERISTIC:
- (A) LENGTH: 253 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74:

```

RSVVRRCLKM AAEPEQQQKQ EPLGSDSEGV NCLAYDEAIM AQQDRIQOEI AVQNPLVSR 60
LELSVLYKEY AEDDNIYQKQ IKDLHKKYSY IRKTRPDGNC FYRAFGFSLH EALLDDSKEL120
QRFKAVSAKS KEDLVSQGFT EFTIEDFHNT FMDLIEQVEK QTSVADLLAS FNDQSTSDYL180
VVYLRLLTSG YLQRESKFFE HFIEGGRTVK EFCQQEVEFM CKESDHIHII ALAQAALSVS1240
QVEYMDRGEG GTT 253

```

(2) INFORMATION ON SEQ ID NO. 75:

- (i) SEQUENCE CHARACTERISTIC:
- (A) LENGTH: 108 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75:

```

EKFLNMGAPL GVGLGLVFVS SIGIYVSSTY PPVAGATLYS VAMYGGVLVF SMELLYDTQK 60
VIKRAEVSPM YGVQKYDPIN SMLSIYMDTL NIFMRVATML ATGNGNRK 108

```

(2) INFORMATION ON SEQ ID NO. 82:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 164 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82:

MHRDSCPLDC KVIYVGNLGN GNKTELEAF GYVGPLRSV VARNPPGF AF VEFEDPRDAA 60
 DAVRELDGRT LCGCRVRVEL SNGEKRSNR GPPPSWGR RP RDYRRRSPP PRRRSPRRS 120
 FSRSRSRSL S RDRRRERSLS RERNHKPSRS FSRSRSRSR S NERK 164

(2) INFORMATION ON SEQ ID NO. 83:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 138 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83:

EAALTLCHELL SSVVSLES LT LSYNGLGSNI FRLLDSLRL SQAGCRLRA LHLSDLFSP L 60
 PILELTRAIV RALPLLRLVLS IRVDHPSQ RD NPGVPGNAGP PSHIIGDEEI PENCLEQLEM120
 XISTGSPASP TAVLRSEGLG FSAAAVPG 148

(2) INFORMATION ON SEQ ID NO. 90:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 145 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 90:

EDGADGAFYP DEIQRPPVRV PSWGLEDNVV CSQPARNFSR PDGLEDSEDS KEDENVPTAP 60
 DPPSQHLRGH GTGFCFDSSE DVHKKCPLCE LMFPNYDQS KFEHVESHV KVCPMCSEQF 120
 PPDYDQQVFE RHVQTHFDQN VLNFD 145

(2) INFORMATION ON SEQ ID NO. 91:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 282 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91:

DKSSACRRNG NYSDEKKDAM YWEKRRKNNE AAKRSREKRR LNDLVLENKL IALGEENATL 60
 KAELLSLKLK FGLISSTAYA QEIQKLSNST AVYFQDYQTS KSNVSSFVDE HEPMSVSSSC120
 ISVIKHSPQS SLSDVSEVSS VEHTQESSVQ GSCRSPEKPF QIIKQEPMEI ESYTREPRDD180
 RGSYTASIYQ NYMGNSFSGY SHSPPLLQVN RSSNSPRTS ETDDGVVVGKS SDGEDEQQVP240

KGPIHSPVEL KHVHATVVKV PEVNSSALPH KLRIKAKAMQ IK 282

(2) INFORMATION ON SEQ ID NO. 92:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 92 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92:

```
MASLGHILVF CVGLLTMAKA ESPKEHDPFT YDYQSLQIGG LVIAGILFIL GILIVLSRRC 60
RCKFNQQQRT GEPDEEEGTF RSSIRRLSTR RR 92
```

(2) INFORMATION ON SEQ ID NO. 93:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 140 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93:

```
WTGTGRGAVA IMADPDPRYP RSSIEDDFNY GSSVASATVH IRMAFLRKVY SILSLQVLLT 60
TVTSTVFLYF ESVRTFVHES PALILLFALG SLGLIFALTL NRHKYPLNLY LLFGFTLLEA 120
LTVAVVVVTS MYILSASFHT 140
```

(2) INFORMATION ON SEQ ID NO. 97:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 51 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97:

```
FFPLLLPLHT PVAGRNLGFP ESLGVPPFLP HPGGTPRAPG LFLLLFSFWA V
```

(2) INFORMATION ON SEQ ID NO. 98:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 53 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 98:

FFLYSFPTFP PWLEGTASL KAWGSHPSYP TREERPGRPA CFSSCFPFQ FDI

53

(2) INFORMATION ON SEQ ID NO. 99:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 52 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 99:

PLDCATFVFV FLNFFKPRMI SPASFSSPSS QTEFKGHFSS SFWHLQPQSG IF

52

(2) INFORMATION ON SEQ ID NO. 100:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 122 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 100:

PFSSSVSFFG TAPSCLEGGW ILVCALDRYR INTCALRTGS PRFIQSAHYR KLLCQNPFGD 60
 PTPGSPSSL TSTRAVLFF ILLFYCFCCG HYHWQSSFSP FLDIGVLSLK DSTLRKVKPK120
 AA 122

(2) INFORMATION ON SEQ ID NO. 101:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 126 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 101:

LLFFFCFLFWD CAIMFIRRLD FGVCQRQIQN KYLRLENRKS TIHTKCSLQE VAVSKSRQGP 60
 NSGQPLLPAD LNKGCAIVFY FIILLLLWS LSLAKFLFPF PGHRGPVFKR FHSEAEGAKS120
 CLRSGL 126

(2) INFORMATION ON SEQ ID NO. 102:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 73 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 102:

IDFEGKERGK GQGRDTPPLP LSWAQKLGGS RERIFTFFKL LFSEWNKLGQ GAQALSSVPH 60
 TPLLRFSIQK NIS 73

(2) INFORMATION ON SEQ ID NO. 103:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 144 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103:

```

ILRGRREGRV RVETPLPCPF PGPRSWGEGG KGFLHFLNCY FLNGTSWAKG PRPCPLSLTP 60
LCVSHSFKKT FLEHLLCPAY ARPTS*VCVG GLYASSSVPP CPSFTGAFGG SVGGGTFCGV 120
WGSPGSPTKL SPSVPVTHLL QPPA                                     144

```

(2) INFORMATION ON SEQ ID NO. 104:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 116 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 104:

```

CRPTIFTPRP PALGEGSTTT SPLDIPLGTG MWVPLTVRPW GEPKALTSGI AMLGGGASET 60
VGRQDILGAA PSQQGIRQGA VGDGLAQGGK TAWSGFLEIP KPHRSSHLLQ IPQRHR 116

```

(2) INFORMATION ON SEQ ID NO. 105:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 22 amino acids
 - (B) TYPE: Protein

- (C) STRAND: individual
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105:

RMGKEALMSW RRDPPHTLSW WA

22

(2) INFORMATION ON SEQ ID NO. 109:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 165 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 109:

GAGPWAEAFPD GIGRRSRRAR LPOYKRPPGG GGGGDSGRRN MAVADLALIP DVDIDSDGVF 60
 KYVLIRVHSA PRSGAPAAES KEIVRGYKWA EYHADIYDKV SGDMQKQGCD CECLGGGRIS 120
 HQSQDKKIHV YGYSMAYGPA QHAISTEKIK AKYPDYEVTW ANDGYL 65

(2) INFORMATION ON SEQ ID NO. 111:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 33 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 111:

PSSPSLPVLR AGLRPFCDVL PGCGCVRFCL SCL

33

(2) INFORMATION ON SEQ ID NO. 112:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 31 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 112:

ETCAGAGRCA ADGGNGSGSR VPPASRCCAL G

31

(2) INFORMATION ON SEQ ID NO. 113:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 67 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 113:

KRAQAPAAAL QMAEMDPVAE FPQPPGAARW AEALLRCFTW LRLCQISMFL SLKCLNTRSS 60
HLGAHCR 67

(2) INFORMATION ON SEQ ID NO. 114:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 246 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 114:

```

GCVAGSAGLS RKSPWTEVET ETFLGSPRYS RRVRSYCYWLL GLMAVRASFE NNCEIGCFK 60
LTNTYCLVAI GGSENFYSVF EGELSDTIPV VHASIAGCRI IGRMCVGNRH GLLVPNNITD 120
QELQHIRNSL PDTVQIARVE ERLSALGNVT TCNDYVALVH PDLRETEEI LADVLKVEVF 180

RQTVADQVLV GSYCVFSNQG GLVHPKTSIE DQDECLSFQV PCCGDVNEAL SDSWDVYNVS 240
FVPETT                                           246

```

(2) INFORMATION ON SEQ ID NO. 116:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 72 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 116:

```

MGYNLSPQFT QLLVSRYPFR SANPAMQLDR FIQVCTQLQV LTEAFREKDT AVQGNIRLSF 60
EDFVTMTASR ML                                           72

```

(2) INFORMATION ON SEQ ID NO. 117:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 35 amino acids
 - (B) TYPE: Protein

- (C) STRAND: individual
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 117:

EHTHRCSQDL RLATVSNSVA SKREYVLCPA IGH LG

35

(2) INFORMATION ON SEQ ID NO. 118:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 40 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 118:

ATLWLAKKEF ICAQPLVTLG DAPDSRQMLV HWPSSSFLK

40

(2) INFORMATION ON SEQ ID NO. 119:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 33 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 119:

QKRSLFVPSH WSPWVMHQIA GRCWFIGLRP LSS

33

(2) INFORMATION ON SEQ ID NO. 120:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 161 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 120:

LSSSRSFIST SWGAFVFFCL LSCGSLVLAG FEGASTSMV FSWASRICW RSFLRFFPDS 60
 VMLARALDAR FLRWCRVISP WSITAPTTTC LRRRSRENTT RRLNSFFFS VRGRLIFPPG 120
 APIVAIPLQF TVRTSAQRRI RGLRPGLPRA NRNSGAGPRA I 161

(2) INFORMATION ON SEQ ID NO. 121:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 49 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 121:

FFQSARALLQ MELTAREALL QSFCTFFFP KDIPLGEVSR PLGRKSGE

49

(2) INFORMATION ON SEQ ID NO. 122:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 25 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 122:

KGALLLSKSS ETTTESEGWL QLRIF

25

(2) INFORMATION ON SEQ ID NO. 123:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 25 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 123:

WKRFSSHLQG PSFLHPGGLL SSFAF

25

(2) INFORMATION ON SEQ ID NO. 124:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 160 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 124:

```

WLLQLKPHLL AHHPKGLPH RGAPLYSPRT RPRVAIGPRK AGAEPADPAL SGSTDRELEW 60
NRDYGSSGGK DQPAPNGAEE EAVQTPAGVE SGAASEAPGG RGC DRPRADH AAPPEAGVQ 120
CTCQHYTVRE EAQKTPPADP ACPEREDSHG SGSPFKASQD                      160

```

(2) INFORMATION ON SEQ ID NO. 128:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 78 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 128:

```

FFPFCQPFIG SGTHEVQLVP GTVHSLKQLK GLSPD TDATL SRMHGPG LTL SMEEVGSARG 60
GRMVARDTES LVLGLNLNLS                                         78

```

(2) INFORMATION ON SEQ ID NO. 129:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 110 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 129:

CALLPPTPSR TEP SLHSTGD SGKGAEDRQE AHRDRPTGSQ AAPEERDIQ TEESLPAPHSF 60
QDEKNLPPPP DTDAREVGGR SGKFPFVPP RTSEPSMLNF FFIKITFIL 110

(2) INFORMATION ON SEQ ID NO. 130:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 102 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 130:

SLPADVPCCP PPHPAQNHPC IPQGRARVP KIDKRHTETD QLAARQPQR ETFRQRKVSL 60
PLIPSKMRKT CRHPPTLMPG RWEEEVGNFP SQYPQERLSL QC 102

(2) INFORMATION ON SEQ ID NO. 131:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 31 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 131:

LCQLMCPVAP HPIPHRTIPA FHRGLQGCR R

(2) INFORMATION ON SEQ ID NO. 132:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 166 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 132:

```

GFRPARCDPV PLPTTRSVAG LPVGRVRQLS RPLLGPDTGS VANIFKGLVI LPEMSLVIRN 60
DQRVIPIRRA PLRSKIEIVR RILGVQKFDL GIICVDNKNI QHINRIYRDR NVPTDVLSP 120
RHEHLKAGEF PQPDFPDDYN LGDIFLGVEY IFHQCREDED YNDVLT 166

```

(2) INFORMATION ON SEQ ID NO. 133:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 244 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 133:

```

FDPKLELEGKV KEDPDQGESM KPLTFARFYL PILVPSAKKA IYMDDDVIVQ GDILALYN 60
LKPGHAAAFS EDCDSASTKV VIRGAGNQYN YIGYLDYKKE RIRKLSMKAS TCSFNP 120
ANLTWKRQN ITNQLEKWMK LNVEEGLYSR TLAGSITTPP LLIVFYQQHS TIDPMW 180
LGSSAGKRY S PQFVKAAKLL HWNGHLKFWG RTASYTDVWE KWIYDPDTGK FNLIRRY 240
SNIK 244

```

(2) INFORMATION ON SEQ ID NO. 134:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 63 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 134:

PSFIIHSNPI WLGALLWVSH CPSSILGSLR PRGGKIQLRV GGSEPCRIMK ATCFGNDLPL 60
 PVV 63

(2) INFORMATION ON SEQ ID NO. 135:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 69 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 135:

DYLRLLSSGFC QNTPLTESTE GMGVGGLGRV RLECEGSLIY AELKSPSLYV HTFVLFSRLI 60
 LAIPNPLPR 69

(2) INFORMATION ON SEQ ID NO. 136:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 47 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 136:

QPFYFNTPL SILHFPPLSK LNLVHRVGLC MCMQEVGVDS ALGWNPP

47

(2) INFORMATION ON SEQ ID NO. 137:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 83 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 137:

VPPCPQLREL CPGVNNQPYL CESGHCCGET GCCTYYYELW WFWLLWTVLI LFSCCCAFRH 60
 RRAKLRLQQQ QRHVEINLLA YHG 83

(2) INFORMATION ON SEQ ID NO. 139:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 88 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 139:

WKSQQLHRML LTRTEFWYLS TEVSTMFTCK RLKKPLKWT GIQSSFSVTH QSDKRLVTL 60
 PGLFSFYNSS SIHNDFVLCS IFFNPLSI 88

(2) INFORMATION ON SEQ ID NO. 140:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 21 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 140:

CYMHFLTFVK NVTIVKKCTK M

21

(2) INFORMATION ON SEQ ID NO. 141:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 58 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 141:

MEIEQVHFPA YRQLYTDLNI FSSCLVKVKE KGFFLPQDIT FFYITSITHH CFWWKSAAE 58

(2) INFORMATION ON SEQ ID NO. 142:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 21 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 142:

NSFLTQMMVL QNNKMAEHFH K

21

(2) INFORMATION ON SEQ ID NO. 143:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 44 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 143:

SVTKSGFLIP CHLGDFILLC CFKIQCREEV DCRGNKVNSN FEKK

44

(2) INFORMATION ON SEQ ID NO. 144:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 67 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 144:

NPPNDKVSEI QTSLSHSICEN VQPFYCSVKE PSSGSKMNSI NQRIFYTLEK KISSNILEY 60
CKLHFSS 67

(2) INFORMATION ON SEQ ID NO. 145:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 65 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 145:

KVHTILHFST KSSGVLCLLY KKKLYPVAGK TLSLSLLINN WRKCSSLYKV AYKLESELVQ 60
SPFTTF 65

(2) INFORMATION ON SEQ ID NO. 146:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 55 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 146:

KIWSREQNHC EWMNCKMKK VQAKLLQVFC HFDESQKMNH GYLSTLRVFS LIFCM

55

(2) INFORMATION ON SEQ ID NO. 147:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 113 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 147:

IPEDPHIDES KAKHQAIIMS TSLRVSPSIH GYHFDASRK KAVGNIFENT DQESLERLFR 60
 NSGDKKAEER AKIIFAIDQD VEEKTRALMA LKRTKDKLF QFLKLRKYSI KVH 113

(2) INFORMATION ON SEQ ID NO. 148:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 88 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 148:

MOHFAATLQA SLLSGLQRLE RDRDWKGTRT EQTGKDSKQ FHALCCYRGE QNAFSKDLKT 60
 LPSLQERIDA DRRATDVMR TKENDGWR 88

(2) INFORMATION ON SEQ ID NO. 149:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 143 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 149:

```
VVEGPDGHH GDAGAEVPRC LWPRSGICGR ECGLGDRWFL RVEDRQDLNR QRIQRYAQAF 60
HTRGSEDLK DSVEKLELGC PFSPLSLPM PSVSRSTSR SANWERLRQG TLRDLRGII 120
NRGLEDGESW EYQI 134
```

(2) INFORMATION ON SEQ ID NO. 152:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 99 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 152:

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MKVSAAALLCL LLIAATFIPQ GLAQPDAINA PVTCCYNFTN RKISVQRLAS YRRITSSKCP 60
KEAVIFKTIV AKEICADPKQ KVVQDSMDHL DKQTQPKT 99
```

(2) INFORMATION ON SEQ ID NO. 154:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 52 amino acids
 - (B) TYPE: Protein

- (C) STRAND: individual
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 154:

VFFETAENWW YFHIHSVSIQ FQYPHLMRKK CFTNEGGILK LAVMLGWRKF GI

52

(2) INFORMATION ON SEQ ID NO. 155:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 25 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 155:

FFFLQKIGG IFTFIVFLSN FSTHI

25

(2) INFORMATION ON SEQ ID NO. 156:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 40 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 156:

ISCNVRLEKI WYLGYPQGTI KSDFCFFVKK NFFNQYCFYK

40

(2) INFORMATION ON SEQ ID NO. 157:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 66 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 157:

NANYCIHHKL KKRTCIRRLK TRKKIQHPNM YSQEGNQFCN RTGIMNYKQE GVEKEEKKMC 60
EFKTL 66

(2) INFORMATION ON SEQ ID NO. 158:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 23 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 158:

PCCEVLAVGV NVWKCSQQVC WGV

23

(2) INFORMATION ON SEQ ID NO. 159:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 67 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 159:

PAVKSWQVLV MCGNAVSKFA GEFDKSIKQN KKSLGILFH DFFCSFTPEG RNGLQQVVEE 60
EGGEQVY 67

(2) INFORMATION ON SEQ ID NO. 160:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 108 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 160:

EGEPACSGIQ ARRVTPCPS RASAPAPASE TSLSVPATLV GGSDLIHFQV GSGPTPGPAE 60
DRAARPSWLT LQLALGWGGR ELMASVASLSW GFPACPVVSC PRCYRGCA 108

(2) INFORMATION ON SEQ ID NO. 161:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: Protein

- (C) STRAND: individual
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 161:

FCSTTSSVAL HQKEGMGYSR

20

(2) INFORMATION ON SEQ ID NO. 162:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 61 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 162:

IPGLKYFVGI AYYIILADEP QDNGYRHTHT YHTKSQLLK SGLGIRLLCP VKNSCTEVIV 60
 T 61

(2) INFORMATION ON SEQ ID NO. 163:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 22 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 163:

LMNLRTTATD THIHTRTQNL SC

22

(2) INFORMATION ON SEQ ID NO. 164:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 37 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 164:

TSGQRLQHT YIHAHKISAV EEWAWNQTSV SSKKLLH

(2) INFORMATION ON SEQ ID NO. 165:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 72 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 165:

TVPFVSASG FHLIFFALPI LFQFVAKNHE TRQWKHRHRR RGPSCALKAG KTASGAGEVV 60
RCLSEQSVAI SR 72

(2) INFORMATION ON SEQ ID NO. 168:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 25 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 168:

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- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 170:

LLACCTETGI TCLQYTNTHM LSFVLFWQLT RS

32

(2) INFORMATION ON SEQ ID NO. 171:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 50 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 171:

IALSCCFNVV HTIASQTCYS SVICSVVTKV TGLVLFAQFL RLVCFHLHLIN

50

(2) INFORMATION ON SEQ ID NO. 172:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 51 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 172:

EHYTIGFQYC THKIHTCVQK VSSSRLVIPF TWKINEGNLY ILYKNKSKFI Y

51

(2) INFORMATION ON SEQ ID NO. 173:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 239 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 173:

LFIFHRNNTN NWREIPENLM DQYSEVNAIS TACSNVPEC EEMVSGLEFKQ WMENPNNNPI 60
 HPNLRSTVYC NAIAQGGEEE WDFAWQFRN ATLNEADKL RAALACSKEL WILNRYLSYT 120
 LNPDLRKQD ATSTIISITN NVIGQGLVWD FVQSNWKKLF NDYGGGSFSF SNLIQAVTRR 180
 FSTEYELQQL EQPKDNEET GFGSGTRALE QALEKTKANI KVVKENKEVV LQWFTENSK 239

(2) INFORMATION ON SEQ ID NO. 183:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 109 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 183:

YANQSSSLRF KIKYKLLCS THSGSIVPEP DCYFFILNII FPHLICLPLI HRHLEKEMGG 60
 CLLSLSLCFV PVVRLAASVA RWAWLEPWVR QVAGGDRERL RGKWWHLLL 109

(2) INFORMATION ON SEQ ID NO. 184:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 33 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 184:

SLFLSSTGVS APLOGQSKSL HPEPPPIPVH FSR

33

(2) INFORMATION ON SEQ ID NO. 185:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 46 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 185:

HSFSARLEFL HLCRGKVSPC TLNHPPFLFI SADNDGGGGV SIVLRV

46

(2) INFORMATION ON SEQ ID NO. 186:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 105 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 186:

VEGTCSDGVF SGFLAPGCAV HRPFRPWFQH PQQGQWKCQS SKCHHFPLSL SLSPPATCLT 60
 HGSNQAHRAT DAASLTGTGK QRERDNRHPP ISFSKCLWMR GRQIR 105

(2) INFORMATION ON SEQ ID NO. 187:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 73 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 187:

RGHAVTEYLV GSLLLAQVFT GPTGLGPSIP SRDSGSRVAV NATTSLSASF CPRQPPASPT 60
 ALTKPTEQLT LPV 73

(2) INFORMATION ON SEQ ID NO. 188:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 28 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 188:

MFIFFFMLSI QALFHGQQVI FHNVDFFK

28

(2) INFORMATION ON SEQ ID NO. 189:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 65 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 189:

HLNTAILWLL LVFLWYVVWE CLWNYQYLKF SKEPWKSITL NESLSLYMNY VLKFDQLSLR 60
 HKTVI 65

(2) INFORMATION ON SEQ ID NO. 190:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 30 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 190:

CFSFFSCYLS KHCSMVSKSY FIMWIFQNNY

30

(2) INFORMATION ON SEQ ID NO. 191:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 41 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 191:

EFFFVTNVFY LFINKKCIVQ ALYPNPSTQK KINNRPWMAQ T

41

(2) INFORMATION ON SEQ ID NO. 192:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 29 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 192:

YKPFPIQVL RKRLTTDPGW HRHNLFGVI

29

(2) INFORMATION ON SEQ ID NO. 193:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 33 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 193:

SSHMTNTYD FSFRNIIRRL NLLQQQKFN PLN

33

(2) INFORMATION ON SEQ ID NO. 194:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 153 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 194:

TPLRKEVLKS KMGKSEKIAL PHGQLVHGIH LYEQPKINRQ KSKYNLPLTK ITSAKRNENN 60
 FWQDSVSSDR IQKQEKKEFK NTNENKNSHL KKSAPLFEVS QKENYAGAKF SDPPSPSVLP 120
 KPPSHWMGST VENSNNQREL MAVHLKTLK VQT 153

(2) INFORMATION ON SEQ ID NO. 195:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 304 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 195:

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SLYYYGIRD L ATVFYFMYLVA IIIHAVIQEY MLDKINRRMH FSKTKHSEFN ESGQLSAFY L 60
FACVWGTFIL ISENYISDPT ILWRAYPHNL MTFQMKFFYI SQLAYWLHAF PELYFQKTKK 120
EDIPRQLVYI GLYLFHIA GA YLLNLNLHGL VLLVLHYFVE FLFHISRLFY FSNEKYQKGF 180
SLWAVLFVLG RLLTLILSVL TVGFGRLARAE NQKLDFTGN FNVLA VRIAV LASICVTQAF 240
MMWKFINFQL RRWRHESAFQ APAVKKKPTV TKGRSSKKG T ENG VNGTLTS NVADSPRNKK 300
EKSS 304

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(2) INFORMATION ON SEQ ID NO. 201:

- (i) SEQUENCE CHARACTERISTIC:
- (A) LENGTH: 198 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 201:

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KMTTAARPTF EPARGGRGKG EGDLSQLSKQ YSSRDLPSTH KIKYRQTTQD APEEVNRNDF 60
RRELEERERA AAREKNRDRP TREHTTSSSV SKKPRLDQIP AANLDADDPL TDEEDDFEE 120
ESDDDDTAAL LAELEKIKKE RAEKGQGPVK GPRAKKALRG GRVSWENIG WAGNPFPLIL 180
SLAHSKLKAD FEKFERRV 198

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(2) INFORMATION ON SEQ ID NO. 202:

- (i) SEQUENCE CHARACTERISTIC:
- (A) LENGTH: 55 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 202:

VLIFLVFLLD GKAVGINRGQ RLMLEWPVEV VEQSSHLLSG AVSGWVYLKA TKCFG 55

(2) INFORMATION ON SEQ ID NO. 203:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 66 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 203:

SPGFFLSLPF STGXAWASSS CHPSRKAPAP SCLPAACIQG QSSGLQTGLV PPPLQGMGVG 60
EGAFKK 66

(2) INFORMATION ON SEQ ID NO. 204:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 161 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 204:

HLGYGKLLWC VVGFLFSFLS FSPFSLLEAF SFPFSPPLAK LGPHPHVILL GRRLPHLVCR 60
QHASKARAQA CRLGWCLLRF RVVELVKGLS KNNKKKKVKS LVASIHSDPG RQQGFVDLDS 120
LGMSSCQPGQ DPGLPRAEAL PATRIPLWLG LCVQRSGSET S 161

(2) INFORMATION ON SEQ ID NO. 205:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 37 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 205:

ID: BLVFIVEH TYQGEVLHTQ LQIFGKKAV KKIQLQLL
 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37

37

(2) INFORMATION ON SEQ ID NO. 206:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 32 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 206:

ID: ENYFAFSVNL RSVLNKQSS ARPFFSLMSA LG
 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32

32

(2) INFORMATION ON SEQ ID NO. 207:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 102 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 207:

CMLQINLYFF PLGFSKNTT STPNEHGTCL FLPLLIYSRF SSVFFSNAAF SCSSGLLSGS 60
 IVAKDSIRST LHSDVKHSHC LDSSSFLSSN SITDKASVLT DE 102

(2) INFORMATION ON SEQ ID NO. 208:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 34 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 208:

VLFSKEYVID LQVSSRISAK ASGSACSSSK SINP

34

(2) INFORMATION ON SEQ ID NO. 209:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 43 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 209:

VAHWQGDQKH YFHTCVMILF FLRESHSVAR LGVQWHDLS LQP

43

(2) INFORMATION ON SEQ ID NO. 210:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 204 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 210:

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DLTFEQIRKL NPAANHRLRN DFPDEKIPTL REAVAECNLH NLTIFFDVKG HAHKATEALK 60
KMYMEFPQLY NNSVVCSELP EVIYKMRQTD RDVITALTHR PWSLSHTGDG KPRYDTFWKH 120
FIFVMDILL DWSMHNILWY LCGISAFMLQ KDFVSPAYLK KWSAKGIQVV GWTVNTFDEK 180
SYYESHLGSS YITDSMVEDC EPHF 204

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(2) INFORMATION ON SEQ ID NO. 214:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 33 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 214:

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SEKVTLLWKSE TRGCHEGSFS FSEKIGMGY RTI

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33

(2) INFORMATION ON SEQ ID NO. 215:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 61 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 215:

NSKVDVIFTP MSICPISVSS SPLGIYSLYV NKIRSSDSL I QSSSFSSLFL CRLLDIYCST 60
 T 61

(2) INFORMATION ON SEQ ID NO. 216:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 24 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 216:

PMYKIAKCLL FIKRCNGVGG RGNF

24

(2) INFORMATION ON SEQ ID NO. 217:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1880 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: partial cDNAs produced from individual
ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 217:

CGCCGGGGGC CGGGGGCGGC CCAGGGGGGG GCCCGGGGCC GGGGCCCTGC CTGAGGCGAG 60
 AGCTGAAGCT GCTCGAGTCC ATCTTGCCAC CGCGGCCACG AGCGCTTCCG CATTGCCAGC 120
 GCCTGCCTGG ACGAGCTGAG CTGCGAGTTC CTGCTGGCTG GGGCCGGAGG GGGCCGGGCG 180
 GGGGCCCGCG CCGGACCGCA TCTCCCCCA CGGGGGTCGG TGCTTGGGGA TCCTGTCCCG 240
 ATCCACTGCA ACATCAGGA GTCATACCTT GCTGTGCCCC CCATCTGGTC GGTGGAGTCT 300
 GATGACCCTA ACTTGGCTGC TGTCTTGGAG AGGCTGGTGG ACATAAAGAA AGGGAATACT 360
 CTGCTATTGC AGCATCTGAA GAGGATCATC TCCGACCTGT GTAACTCTA TAACCTCCCT 420
 CAGCATCCAG ATGTGGAGAT GCTGGATCAA CCTTGCCAG CAGAGCAGTG CACACAGGAA 480
 GACGTGTCTT CAGAAGATGA AGATGAGGAG ATGCTGAGG ACACAGAAGA CTTAGATCAC 540
 TATGAAATGA AAGAGGAAGA GCCAGCTGAG GGCAAGAAAT CTGAAGATGA TGGCATTGGA 600
 AAAGAAAAC TGGCCATCCT AGAGAAAATT AAAAAGAACC AGAGGCAAGA TTACTTAAAT 660
 GGTGCAGTGT CTGGCTCGGT GCAGGCCACT GACCGGCTGA TGAAGGAGCT CAGGGATATA 720
 TACCGATCAC AGAGTTTCAA AGGCGGAAAC TATGCAGTCG AACTCGTGAA TGACAGTCTG 780
 TATGATTGGA ATGTCAAAT CCTCAAAGTT GACCAGGACA GCGCTTTGCA CAACGATCTC 840
 CAGATCCTCA AAGAGAAAAGA AGGAGCCGAC TTCATTCTAC TTAACCTTTC CTTTAAAGAT 900
 AACTTTCCCT TTGACCCACC ATTTGTGTCAG GTTGTGTCTC CAGTCCCTCTC TGGAGGGTAT 960
 GTTCTGGGCG GAGGGGCCAT CTGCATGGAA CTTCTACCA AACAGGGCTG GAGCAGTGCC1020
 TACTCCATAG AGTCAGTAT CATGCAGATC AGTGCCACAC TGGTGAAGGG GAAAGCACGA1080
 GTGCAGTTTG GAGCCAACAA ATCTCAATAC AGTCTGACAA GAGCACAGCA TCCTACAAG1140
 TCCTTGGTGC AGATCCACGA AAAAACCGGC TGGTACACAC CCCCCAAAAGA AGACGGCTAA1200
 CCCTGGAGTA TCACCCCTCC TCCCTCCCCA GGCACCAC TG ACCAATTAC CTTTGAATGC1260
 TGTATTTGGA TCTCACGCTG CCTCTGTGGT TCCCTCCCTC ATTTTTCCTG GACGTGATAG1320
 CTCTGCCTAT TGCAGGACAA TGATGGCTAT TCTAAACGCT AAGGAAAAAA AACAAACACA1380
 GAAGTGTTTC AAGTACTCAA GACTGACTTA CAGACCAACC AACCACCTTG CTGGAACCTT1440
 TGCTAGCAGG CATTCTTATA AAAGAAACTT TCGAGCCTCC TTATATTGCT GGAACCTCAG1500
 CTGTGCTCCA GACTAGAGCC TCCTTACCTA TGCTATGGAT TTTTAATTTA TTTCTCTTA1560
 TTTCAITGAC ACTGCTTTTT TTGGTTACAG TGTATGATGG ATGTGTATGA AAAAAATGTA1620
 TCTTTGGGAA AACAATTACA GTTTGTTAAT TTGGAAAAAA AAAAAATGAC TCATCTTTAT1680
 TTTTATTCGC ACATCCACCC CCATCCCCCTG GAACCTACTG GGGAGGTGGG GAGGGGTACG1740
 AGTCCACTGT TGCTTTGGTA GGAGATGAGA GGGCGCATTT GCTGCTTAAG CAAGGGGAAC1800
 TGGGGCTGAG CACACACCGG GGTGCCCCCG GATTTTTCCT CAAGGGCTCT GGAGCACGG1860
 CACCGGCCCC TTGGGATGCA 1880

(2) INFORMATION ON SEQ ID NO. 218:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1024 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 218:

```

GCGGTCGGTA GTGCGGCGCT GTTAAAGAT GCGGCGGAG GAACCTCAGC AGCAGAAGCA 60
GGAGCCGCTG GGCAGCGACT CCGAAGTGTT AACTGTCTGG CCTATGATGA AGCCATCATG 120
GCTCAGCAGG ACCGAATTCA GCAAGAGATT GCTGTGCAGA ACCCTCTGGT GTCCAGAGCGG 180
CTGGAGCTCT CGGTCTTATA CAAGGAGTAT GCTGAAGATG ACAACATCTA TCAACAGAAG 240
ATCAAGGACC TCCACAAAAA GTACTCGTAC ATCCGCAAGA CCAGGCCCTGA CGGCAACTGT 300
TTCTATCGGG CTTTCGGATT CTCCCCTTG GAGGCACTGC TGGATGACAG CAAGGAGTTG 360
CAGCGGTTCA AGGCTGTGTC TGCCAAGAGC AAGGAAGACC TGGTGTCCCA GGGCTTCACT 420
GAATTCACAA TTGAGGATTT CCACAACACG TTCATGGACC TGATTGAGCA GGTGGAGAAG 480
CAGACCTCTG TCGCCGACCT GCTGGCCTCC TTCATGACC AGAGCACCTC CGACTACCTT 540
GTGGTCTACC TGGGCTGCT CACCTCGGGC TACCTGCAGC GCAGAGCAA GTTCTTCGAG 600
CACTTCATCG AGGGTGGACG GACTGTCAAG GAGTCTGCCC AGCAGGAGGT GGAGCCCATG 660
TGCAAGGAGA GCGACCATAT CCACATCATT GCGCTGGCCC AGGCCCTCAG CGTGTCCATC 720
CAGGTGGAGT ACATGGACCG CGGCGAGGGC GGCACCACCA ATCCGCACAT CTTCCCTGAG 780
GGCTCCGAGC CCAAGGTTCTA CCTTCTCTAC CGGCCTGGAC ACTACGATAT CCTCTACAAA 840
TAGGGCTGGC TCCAGCCCGC TGCTGCCCTG CTGCCCCCCT CTGCCAGGCG CTAGACATGT 900
ACAGAGGTTT TTCTGTGGTT GTAAATGGTC CTATTTCACC CCCTTCTCC TGTCACATGA 960
CCCCCCCCCA TGTTTTATTA AAGGGGGTGC TGGTGGTGAA AAAAAAAAAA AAAAAAAAAA 1020
AAAA                                              1024

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(2) INFORMATION ON SEQ ID NO. 219:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2383 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 219:

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CCCTTCATTA AAGCCCTCCT AAATATAACT CTTCTGTATC AAAGGACTTA CAAATGTCTC 60
AAGAAAGTAA TGGTGTAGCA GTGTAAGAGA AGTAAAGTC TGCTAGGGGA AACTAATGAA 120
GCATTTTCCT CATTCACATT TTGGGTTGAT ATATTTCATT AAGACAGAAC TAGTCTCTGT 180
TTGCTTTGCT TTTTAGTGCT TAGTCTGAGA GGCAATGCGA GAAACCAAAA GTCTTAGGAG 240
AAAAACTGCT TTCATAATTT CCAGTGTAAG CCACAAAGAA GCTTTTCAT AAAGGCTTGA 300
AAGCTTGAAG AGGTGACAAG AGCAAGCTGT ATTCATTAG ACAGTTCAAT AAATATGCAA 360
AAATAAAAAA ACACCTTATCA ATCATGAGTA TACTGTTTGT ATTCGGAAA AAGCAACATA 420
TTTCATGCTT TGAATATTTT CTCTTGAGAA TAGTTTTAAA GTTATTTCCCT TTGTGAACAT 480
TCAAAAGTAA AACACACATA TATAATTCCA TCAAGGATTC TCTGTATGAT TAACATTCTG 540
TACAAGTCAA ACATGACCAC ATCTATATTG GAAAGAGAGC ACTGAGAAGC AACAGCAGGA 600
GAATGCATCA CCTGTGCTCT TTTCAGGATG AACAGTTTTG TTAAGTTCAG CAGATGAATG 660
TAACAATGAC CACTTGTTTC CAAATACCCA GATGTTTTCT ACTGGCTCCT CACTAATCAA 720
TAACACAAGT GCTAAGTTCT AAGTATTTAA AAAAACAAAA GACTGCGAGT GACTCCTTCT 780
CTCTGGTCCC TTACCAAAAG CTCCAAATCA CTTATGACAT TAATTACAAT ATTCTGCAT 840
CCAAAAAAT ATGCAAAAC AGGTTTGCTA AATTTTAGTT ACTCAGTGAA CCACTAAT 900
TTTAAAGTAG AAAAAAGACT TACATTCTCA TGACACAAAC TTTAGTTTTC ACATTACCA 960
AAACATTTTA AAATCACTCA AACATGAGAA TTGAAATGT GTGTGCTTAT TTGGGAGAGG 1020
ATTACTGCAT TTATCTCCCA GAAAAAAGG CAGACCTGAG GCATCAGAA ATCGGGAACAT 1080
TTAAATATGA TGACATGTTT CTTATCTTCT AAACCTCAAC GAAAGCTGCT TGTACAAACT 1140
ATTTAATGCA TATCTGCCCC ATTAACAAG ATATTGATG TAGCAGAGAA GCCAGAAAGCT 1200
GAGTCACTTC ATTTCTTTCT GTTGCCCTCA GTTGCCAGCA TAGTTGCAAC TCGCATAAAT 1260
ATATTTAATG TATCCATGTA GATACTCAGC ATCAGGTTAA GGGATCATA TTTTGAATCT 1320
CCATACATTG GTGATACTTC GTACGCTTG ATTACTTTCT TGGTATCATA CAGAAGGAAC 1380
ATGCTGAAAA GAACTAATCC ACCGTACATT GCCACTGAGT AAAGAGTGGC ACCAGCCACG 1440
GGTGGTAGGT GGAAGAAACA TAGATCCCAA TGAGGACAGA AAGACGAGAC CCAGGCCACG 1500
TCCACGGGGT GCACCACTGT TCAGAAACCTT TTAAGTGGGC GCACACATGG CCACATGG 1560
GAGGCTCCTC ACAAAGCCAG CTGTGTACCA TGCAGCTCTG ATGAGAAGAG GACCCCTTAA 1620
TATGTGTCGA GGAGCCACCA CTCACCCAT CACACCGAA TGTAGTAACC AAGCAAGATG 1680
CTTTGGGCCCT GGGCTCTGGT CATATGGTAT TGATCGTACC AGCATTCAGC TCCCAACCAT 1740
GGCTGCAAAG GTCAACCCAA TTGTCAACCA AGAGCCTCTC ATCATGAAGT CTATGAGAAC 1800
AGGGCTTCTG CTGATTGCTA GTGAGACAAA AGCTGTTAAA CCAATACTTC CTGTAAGTA 1860
CATATAGGTT GAATGAATTC TATCCTTGAC ATACTGAGGC CAAATATACG CCTTTTCAAT 1920
AGCTCCCAAT TCATTAGACA GTCCCAAGCC ATAGTAGCAC AATGCTCCAA GACCAAGATG 1980
AGGCCCTCCA GCAACAAACC ATCTTCCCAT CTGATCAATT TTAATATTT TTTCATCGA 2040
TGGTTCCAAT GTGCTCTTGT TGAGTTCTTG GCCAGTCTC CACGCGCGGA TCCCAATCT 2100
TGTTTTGGTG GCATATTCCT TGCTAGGTGT TAACAGCCAT TGATTTCTCG TGATGGAAT 2160
GTCACACAAA GGGGAGGCTT TGGTGAAAGC ACCCTAGAAG GTAGTGTCTG 2220
GAGACACACC AGCCTTGCAG CCAACATGGT GGTGGTGAC AGGCTTACG GATGAGATCT 2280
GAAATGCTCG GTCCCGGCT ACCTTCGCCT CGCAGTTTCC CTTCCGGGCC CCTGAGCTG 2340
GCCTCAAAGA GCACAGTTTC TCCGCGCAC TGCAATGTCC AAC 2383

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(2) INFORMATION ON SEQ ID NO. 220:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 3210 base pairs
 (B) TYPE: Nucleic acid
 (C) STRAND: individual
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 (A) ORGANISM: HUMAN
 (C) ORGAN:
- (vii) OTHER ORIGIN:
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 220:

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GCAAGGCTTA CTGTCGGCTG GGAGGGGAGG TGTAGCCGGT CTTTGGGGGT AGGCGGTAGT 60
GGCGGAAGAG GTTCGCGCGC TGATGGCGGA TCAGGATCGG AAGCCTGCGT AACTTTCTCT 120
CTTGATCCGG GAGTCTTTCC ACTGGATTCA CAATGACATC CTTTCAAGAA GTCCCATTCG 180
AGACTTCCAA CTTTGGCCAT GTCATCTTTC AAAATGTGGC CAAGAGTTAC CTTCTTAATG 240
CACACCTTGA ATGTCATTAC ACCTTAATC CATATATTCA TCCACATCCA AAAGATTGGG 300
TTGGTATATT CAAGGTTTGA TGGAGTACTG CTCGTGATTA TTACACGTTT TTATGGTCCC 360
CTATGCTTGA ACATTATTGT GAAGGATCAA CAGTCAATTG TGTACTAGCA TTCCAAGGAT 420
ATTACCTTCC AAATGATGAT GGAGAAATTT ATCAGTTCGT TTACGTTACC CATAAGGGTG 480
AAATTCGTGG AGCAAGTACA CCTTTCAGT TTCGAGCTTC TCTCCAGTT GAAGACTGCG 540
TTACTATGGA AGATGAAGCA AATTCGTACA TGTTAGTGGT GACCACAAAA GCAGGCCCTT 600
TTGAGTTGAA AATTGAGAAA ACCATGAAAG AAAAAGAAGA ACTGTTAAAG TTAATTGCCG 660
TTCTGGAATA AGAAACAGCA CAACCTCGAG AACCAAGTTGG GAGAATGGAA AGAGAACCTT 720
ACCATGAGAA AGAAAGATGT GACCAACTGC AAGCAGAACA AAAGGGTCTT ACTGAAGTAA 780
CACAAAGCTT AAAAATGGAA AATGAAGAG TTAAGAAGAG GTTCAGTGAT GCTACATCCA 840
AAGCCCATCA GCTTGAGGAA GATATTGTGT CAGTAACACA TAAAGCAATT GAAAAAGAAA 900
CGAATTAGA CAGTTTAAAG GACAAACTCA AGAAGGCACA ACATGAAAGA GAACAACTTG 960
AATGTCAGTT GAAGACAGAG AAGGATGAAA AGGAACTTTA TAAGGTACAT TTGAAGAATA1020
CAGAATAGA AATATACCAAG CTTATGTCAG AGGTCCAGAC TTTAAAAAAT TTAGATGGGA1080
ACAAAGAAAG CGTGATTACT CATTTCAAAG AAGAGATTGG CAGGCTCGAG TTATGTTTGG1140
CTGAAAAGGA AAATCTGCAA AGAACTTTCC TGCTTACAAC CTCAGTAAA GAAGATACTT1200
GTTTTTTTAA GAGCAACTT CGTAAAGCAG AGGAACAGGT TCAGGCAACT CGGCAAGAAG1260
TTGTCTTTCT GGCTAAAGAA CTCAGTGATG CTGTCAACGT ACGAGACAGA ACGATGGCAG1320
ACCTGCATAC TGCACGCTGT GAAAACGAGA AAGTGAAAAA GCAGCTTAGCT GATGCAGTGG1380
CAGCACTTAA ACTAAATGCT ATGAAAAAAG ATCAGGACAA GACTGATACA CTGGAACACG1440
AACTAAGAA AGAAGTTGAA GATCTGAAAC TCCGCTCTTCA GATGGCTGCA GACCATTATA1500
AAGAAAAATT TAAAGGAATG CAAAGGCTCC AAAAACAAAT AAACAAACTT TCAGATCAAT1560
CAGCTAATAA TAATAATGCT TTCAACAAGA AAACGGGGAA TCAGCAGAAA GTGAATGAT1620
CTTCAGTAAA CACAGACGCC GCCACTTCTG CCTCTACTGT AGATGTAAAG CCATCACCTT1680
CTGCAGCAGA GGCAGATTTT GACATAGTAA CAAAGGGGCA AGTCTGTGAA ATGACCAAG1740
AAATTTGCTGA CAAACAGAAA AAGTATAATA AATGTAAACA ACTCTTGCAG GATGAGAAAG1800
CAAAATGCAA TAAATATGCT GATGAACCTG CAAAATGGA GACTGAAATG AAAGAACAG1860
TGAAAATTGC TGAAAATGTA AAACCTTGAA TAGCTGAAGT ACAGGACAAT TATAAGAAC1920
TTAAAAGGAG TCTAGAAATAT CCAGCAGAAA GGAATAAGGA AGATGGAGCA GATGGTGC1980
TTTACCAGCA TGAATACACT AGGCCACCTG TCAGAGTCCC CTCTTGGGGA CTGGAAGACA2040
ATGTTGCTCT GAGCCAGCCT GCTCGAAACT TTAGTCGGCC TGATGCTGCTA GAGGACTCTG2100
AGGATAGCAA AGAAGATGAG AATGTGCCTA CTGCTCCTGA TCCTCCAAGT CAACATTATC2160

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GTGGGCATGG GACAGGCTTT TGCTTTGATT CCAGCTTTGA TGTTCACAAG AAGTGTCCTCC2220
TCTGTGAGTT AATGTTTCCCT CCTAACTATG ATCAGAGCAA ATTTGAAGAA CATGTTGAAA2280
GTCACCTGGAA GGTGTGCCCC ATGTGCAGCG AGCAGTTCCC TCCTGACTAT GACCAGCAGG2340
TGTTTGAAG GCATGTGCAG ACCCATTTTG ATCAGAAATGT TCCTAAATTT GACTAGTTAC2400
TTTTTATTAT GAGTTAATAT AGTTTAGCAG TAAAAAAAAC CACACCTAAA2460
ATAGACCACT GAGGAGACCA TAGAGCGGAT GCTTTCATGC ACCCTTTACT GCACCTTCTG2520
ACCAGGAGCT ACTTTGAGTT TGGTGTTACT AGGATCAGGG TCAGTCTTTG GCTTATCAAT2580
AAATTTTAA CTCTGTTAAT CTTACCTGCT TAAAAAAAAC GTTCTTGTTG GTTCGTATCT2640

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TTATTTATTC CTAAGTTTGC AGAACTGTCT GAATAAAGGA TACAAGGATT ATTTCAATGT2700
TACTGCACTG AAAAACGTGT ATGTATTAGT GTGCTAGATT ATTTAGCAGA ATATTACAA2760
GTTTCTGTTG ACCCTGTTGA TTGAGCATGA CTACTAAATA TTATGTAATA AAAAGCATT2820
GTCATAACAG TCTTATGAAG TAGTTCCTCG AATATAGAAA GTTCTATAAT TTAGCCCATG2880
AAATGATAGG TTTTAAATTT TCAGAAATGG AGCTGCATGT AGAATGAGAT CACATGCTTT2940
TATATGTGAA ATATTGGTTT TAGCAATTA CAGAAAGCAT ACTTTGCTAA TTTTATGGCA3000
AAATTTTGA ATAACCTGAA TGATTATTTT TAAACTATCT TGAAGTTGTA TGTATATATC3060
CTAATGGGGA AATGGGGCAA GGGATTGTCA GTATAATTGT TTTCCCGATT AAATGGTCCC3120
CATAACCAGG GGGTGTTTGT GGCATAAAAA TCCATAGGGT ATATAGCAGG ACCCTTTTGT3180
CATTTCCCTG TGGGGATTTA ATTTGGAATT

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3210

(2) INFORMATION ON SEQ ID NO. 221:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1030 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 221:

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CCGCTTTTCTC CGCCCGACGTG GAATTTTGA AGCGAGAAAA TCGACTCGCT CCGTGTTCGC 60
CCGCCGACGC CGCACGCGTTG CTGGGGCTGG GCTCTTCCTC GCGGAAGTGG GGAGGAGGCG 120
GTTGCGGTTA GTGGACCGGG ACCGGTAGGG GTGCTGTTGC CATCATGGCT GACCCCCACC 180
CCCCGTACCC TCGCTCCTCG ATCGAGGACG ACTTCAACTA TGGCAGCAGC GTGGCCCTCCG 240
CCACCGTGCA CATCCGAATG GCCTTTCTGA GAAAAGTCTA CAGCATTCTT TCTCTGCAGG 300
TTCTCTTAAC TACAGTGACT TCAACAGTTT TTTTATACTT TGAGTCTGTA CGGACATTG 360
TACATGAGAG TCCTGCCTTA ATTTTGTGTG TTGCCCTCGG ATCTCTGGGT TTGATTTTGTG 420
CGTTGACTTT AAACAGACAT AAGTATCCCC TTAACCTGTA CCTACTTTTT GGATTTACGC 480
TGTTGGAAGC TCTGACTGTG CAGAGTTGTTG TTACTTTCTA TGATGTATAT ATTATTCTGC 540
AAGCTTTTCA ACTGACTACT ACAGTATTTT TTGGTTTGAC TGTGTATACT CTACAATCTA 600
AGAAGGATTT CAGCAAAATTT GGAGCAGGGC TGTTTGCTCT TTTGTGGATA TTGTGCCTGT 660
CAGGATTCTT GAAGTTTTTT TTTTATAGTG AGATAATGGA GTTGGTCTTA GCCGCTGCAG 720
GAGCCCTTCT TTCTGTGGA TTCATCATCT ATGACACACA CTCACTGATG CATAAACTGT 780
CACCTGAAGA GTACGTATTA GCTGCCATCA GCCTCTACTT GGATATCATC AATCTATTCC 840
TGCACCTGTT ACGGTTTCTG GAAGCAGTTA ATAAAAAGTA ATTAAGAATA TCTCAGCTCA 900
ACTGAAGAAC AACAAAAAAA ATTTAACGAG AAAAAAGGAT TAAAGTAATT GGAAGCAGTA 960
TATAGAAACT GTTTCATTAA GTAATAAAGT TTGAAACAAT GATTAATAAA AAAAAAAA1020

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(2) INFORMATION ON SEQ ID NO. 222:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1216 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 222:

```

TCTGTTCTGT  GGACAACTGT  TACTGTTCTT  CCGTGGCCAA  CCATGGCGGC  CACCAGCCCT  60
ACCCCCGCTC  CGGCCACTTT  CCTGGACAG  TGCCCTCGCA  GGAGTACTCA  CACCCGCTCC  120
CGCCACACCC  CTCGGTCCCC  CAGTCCCTTC  CCAGCCTGGC  GGTCCAGAGAC  TGGCTTGACG  180
CCTCCACAGC  GCCCGGCCAC  CAGGATTTCT  ACAGGGTGTA  TGGGCAGCCG  TCCACCAAC  240
ACTACGTGAC  GAGCTAACGC  CACGCAGGCG  GCGGGGCGCT  GGGGAATCTT  CCTCCCCAGC  300
CCCCGGGCTC  GGGAGTTATG  CATCCAGAGA  CCTGCCCTTC  TACCTTCCTC  GCCTCCCCTC  360
TTCCTCATTC  CATTGCCCCA  GGTCTTTTCC  TTTTGGATT  TGTTTTGGT  TTGGCTTTGT  420
TTTTGATTTT  TTTTATTAT  GAATCTCCTG  GACGCAGAGG  TGACAGTGGG  AGCTGGCCTG  480
GGCCAGGACG  GCAGGTGGCC  CTGGAGATGG  GAAAGTGTCT  GTGTCGAGGC  GCTGAGCTCT  540
CTCTCTGT  CTCCTTTTTT  CCTCTACTCC  TTCCCTTCA  CACCCCGTG  GCTGGAAGGA  600
ACCTCGGCTT  CCCTGAAAGC  TTGGGGGTCC  CACCCTTCTT  ACCCCACCCG  GGAGGAACGC  660
CCAGGGCCCC  GGGCTTGTTT  CTCTCTTGT  TTCTCTTTG  GGCAGTTTGA  TCACGTATCG  720
AGTAAGGAAT  GACCTTTAGA  TTGTGCGACT  TTTGTTTTTG  TTTTTTTAAA  TTTTTTTAAA  780
CCAAGAATGA  TTTCTCCTGC  TTCCTTCTCC  TCACCATCTT  CCCAGACGGA  GTTCAAAGGC  840
CACTTCTCAA  GCAGCTTTTG  GCACCTTCAG  CCTCAGAGTG  GAATCTTTTA  AAGACAGGAC  900
CCCTATGTCC  AGGAAAGGGG  AAAAGGAACT  TTGCCAATGA  TAGTGACCAC  AGCAAAAGCA  960
ATAAAATAAT  AAAATAAAAA  ACAATAGCAC  AGCCCTTGT  GAGGTCAGCA  GGGAGGAGGG  1020
GCTGCCCGGA  GTGGGTCTCT  TGCTTGATT  TTGACACAGC  AACTTCTGT  AGTGAGCACT  1080
TTGTATGAAT  CGTGGACTTC  CTGTCTCAA  GGCGCAGGTA  TTTATTCTGT  ATCTGTCTAG  1140
AGCACACACC  AAAATCCAAC  CTCTAATAA  ACATGATGGC  GCAGTCCCAA  AAAAAAGAAA  1200
CAGAAGAAGA  AAAGGG

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1216

(2) INFORMATION ON SEQ ID NO. 223:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2369 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 223:

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CGGGCGCCCCG  GGGCAGAGTC  CGGCCGGAGC  GGAGGAGCCC  GGCCCCAGGG  ACAGCTCGGC  60
CGTCATTACT  CAGATCAGCA  AGGAGGAGGC  TCGGGGCCCG  CTGGGGGGCA  AAGGTGACCA  120
GAAGTCAGCA  GCTTCCCAAG  AGCCCCGAAG  CCGGGGCATC  CTCACCTCAC  TCCTCTGCTG  180
TGCTGCGCGG  GATGATGGG  AGGCCCTGCC  TGCTCACAGC  GGGGCGCCCC  TGCTTGTTGA  240
GGAGAATGGA  GCCATCCCTA  AGACCCCACT  CCAATACCTG  CTCCTTGAGG  CCAAGGCCCA  300
GGACTCAGAC  AAGATCTGG  TGGTCATCGA  CCTGGACGAG  ACCCTGTGTG  ACAGCTCTCT  360
CAAGCCAGTG  AACACGCGG  ACTTCATCAT  CCCTGTGGAG  ATTGATGGGG  TGGTCCACCA  420
GGTCTACGTG  TTGAAGCGTC  CTCACGTGGA  TGAGTTCTCT  CAGCGAATGG  GCGAGCTCTT  480
TGAATGTGTG  CTGTTCACTG  CTAGCCCTGC  CAAGTACGCA  GACCAGTAG  CTGACCTGCT  540
GGACAAATGG  GGGGCGTTCC  GGGCCCGGCT  GTTTCGAGAG  TCCTGCTCT  TCCACCGGGG  600
GAACTACGTG  AAGGACCTGA  GCCGGTTGGG  TCGAGACCTG  CGGGGGGTGC  TCATCCTGGA  660
CAATTCACTT  GCCTCCTAT  TCTTCCATCC  AGACAAATGCT  GTACCGGTGG  CCTCGTGGTT  720
TGACAACATG  AGTGACACAG  AGCTCCACGA  CCTCTCCGCC  TTCTTCGAGC  AACTCAGCCG  780
TGTGGACGAC  GTGTACTCAG  TGCTCAGGCA  GCCACGGCCA  GGGAGCTAGT  GAGGGTGATG  840
GGGCCAGGAC  CTGCCCCCTG  CCAATGATAC  CCACACCTCC  TCCCAGGAAG  ACTGCCCAGG  900
CCTTTGTTAG  GAAAACCCAT  GGGCCGCGCG  CACACTCAGT  GCCATGGGGA  AGCGGGCGTC  960
TCCCCACCA  GCCCCACCAG  GCGGTGTAGG  GGCAGCAGGC  TGCACTGAGG  ACCGTGAGCT  1020
CCAGGCCCGG  TGTCAGTGCC  TTCAAACCTC  CTCCCCTATT  CTCAGGGGAC  CTGGGGGGCC  1080
CTGCCTGCTG  CTCCCTTTTT  CTGTCTCTGT  CCATGCTGCC  ATGTTTCTCT  GCTGCCAAAT  1140
TGGGCCCCCT  GGGCCCTTCC  GGTTCGTGCT  CCTGGGGGCA  GGGTTCTCTG  CTTGGACCCC  1200
CAGTCTGGGA  ACGGTGGACA  TCAAGTGCTT  TGCATAGAGC  CCCTCTTCC  CCGCCAGCT  1260
TCCCCAGGG  CACAGCTCTA  GGCTGGGAGG  GGAGAACCAG  CCCCTCCCC  TGCCCCACCT  1320
GCTCCCTTGG  GACTGAGAGG  GCCCTACCA  ACCTTTGCC  CTGCTTGGA  GGGAGGGGAG  1380
GTCTGTATCC  ACTGGGGAAG  GCAGCAGGAG  TCTGTCTTCT  AGGCCCCACA  GTGCAGCTTC  1440
TCCAGGGCCG  ACAGCTGAGG  GCTGCTCCCT  GCATCATCCA  AGCAATGACC  TCAGACTTCT  1500
GCCCTTAACA  GCCCCGGGGG  TTGGCTCCCC  CAGCTCTGAG  CGTGGGGGCA  TAGGCAGGAC  1560
GCCCCTGTG  GTGCCATATA  AATATGTACA  TGTGTATATA  GATTTTTAGG  GGAAGGAGAG  1620
AGGGAAGGGT  CAGGGTAGAG  ACACCCCTCC  CTTGCCCTTC  TCCTGGGCCC  AGAAGTTGGG  1680
GGGAAGGAGG  GAAAGGATTT  TTACATTTTT  TAAACTGCTA  TTTTCTGAAT  GGAACAAGCT  1740
GGGCCAAGGG  GCCCAGGCC  TGTCTCTGT  CCTCACACC  CCTTTGCTCC  GTTCATTCAT  1800
TCAAAAAAAT  ATTTCTTGAG  CACCTTCTGT  GCCCAGCATA  TGCTAGGGCC  ACCAGCTAAG  1860
TGTGTGTGGG  GGGTCTCTAC  GCCAGCTCAT  CAGTGCTCTC  TTGCCACTCC  TTCACCGGTG  1920
CCTTTGGGGG  ATCTTAGGA  GGTGGGACCT  TCTGTGGGGT  TTGGGGATCT  CCAGGAAGCC  1980

CGACCAAGCT  GTCCCCCTCC  CCGTGCCAA  CCCATCTCT  ACAGCCCCCT  GCCTGATCCC  2040
CTGCTGGCTG  GGGGCAGCTC  CAGGATATC  CTGCCCTCCA  ACTGTTTCTG  AAGCCCCCTC  2100
TCCTAATCG  CGGATTCGCG  AGGTCAAGGC  TGTGGGCTCT  CCCCAGGGTC  TAACGGTTAA  2160
GGGACCCAC  ATACAGGTGC  CAAGGGGGAT  GTCAAGTGGT  GATGTCGTTG  TGCTCCCTCT  2220
CCCCAGAGG  GGTGGCGGG  GGGTGAATAT  GGTTCGCTG  CACTAGGTGG  CCTTCCCAT  2280
TAAGTGCTT  CTCTGTGACT  GAGAGCCCTA  GTGTGATGAG  AACTAAAGAG  AAAGCCAGAC  2340
CCCTAAAAAA  AAAAAA      AAAAAAA

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2369

(2) INFORMATION ON SEQ ID NO. 224:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 849 base pairs
 (B) TYPE: Nucleic acid
 (C) STRAND: individual
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 (A) ORGANISM: HUMAN
 (C) ORGAN:
- (vii) OTHER ORIGIN:
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 224:

CGAAACGTGC	GCAGGCGCCG	GCCGCTGCGC	TGCAGATGGC	GGAAATGGAT	CCGGTAGCCG	60
AGTTCCCCCA	GCCTCCCGGT	GCTGCGCGCT	GGGCTGAGGC	CCTTCTGCGA	TGTTTTACCT	120
GGCTGCGGCT	GTGTGAGATT	TCTATGTTCC	TGTCCTGAA	ATGCCCTGAAC	ACAAGATCCA	180
GTCATCTGGG	GGCCCACTGC	AGATAACAAT	GAAGATGGTG	CCAAAACCTGC	TTTCTCCTTT	240
GGTTAAAGAT	TGGGCTCCCA	AAGCATTTAT	AATTTCCCTTT	AAGTTGGAGA	CTGACCCCGC	300
CATTGTAATT	AATCGAGCTC	GGAAGGCTTT	GGAAATTTAT	CAGCATCAAG	TGGTGGTGGC	360
TAATATCCTT	GAGTCACGAC	AGTCCTTTGT	GTTTATTGTA	ACCAAAGACT	CGGAAACCAA	420
GTTATTGCTA	TCAGAGGAAG	AAATAGAAAA	AGGCGTAGAG	ATAGAAGAGA	AGATAGTGGA	480
TAATCTTCAG	TCTCGACACA	CAGCTTTTAT	AGGTGACAGA	AACTGAAGTA	AAAAGCCCTT	540
ATAGGATCAA	AAATTGTTCA	GGGCTCTTAG	AGATGGTGAA	AACTACAAAA	AAAACCATGG	600
CTTTCATATG	GACAGATAAA	ATGAAAGAGA	GGGAAAAGGC	AGTGGTGTGT	AGGCAATAT	660
GGTTTGGCAT	TTGTCTTTTA	ATGACACCTG	ATATGATGTC	ATTTTGATTT	TGAAATTGAA	720
CACTAGAACT	GTTAATCACC	TTTAAAAAGG	AAGAGCTTAT	TGGGGATTAT	ATATTCCTTA	780
AAAATATACA	TGGGGGCGCTG	AATGTCAGCC	ATCTGTATAC	TGTGGGGAAA	AGGGGTTTGG	840
GTGCAATTC						849

(2) INFORMATION ON SEQ ID NO. 225:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 1502 base pairs
 (B) TYPE: Nucleic acid
 (C) STRAND: individual
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 (A) ORGANISM: HUMAN
 (C) ORGAN:
- (vii) OTHER ORIGIN:
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 225:

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CCTTACCGGC AGGGCTGCCC AGGAGCTGCA GGACAAGCAC CAGGAGCCCC TCCGGGTAGC 60
TACTACCCCTG GACTCCCCCTC TGGAACTCCA GGAGGACCAT ATGGCGGTGC AGCTCCCGGG 120
GGCCCCATCG GTCAGCCACC TCCAAGTTCC TACGGTGCCC AGCAGCCTGG GCTTTATGGA 180
CAGGGTGGCG CCCCTCCCAA TGTGGATCCT GAGGCCTACT CCTGGTTCCA GTCGGTGGAC 240
TCAGATCACA GTGGCTATAT CTCATGAAG GAGCTAAAGC AGGCCCTGGT CAACTGCAAT 300
TGGTCTTCAT TCAATGATGA GACCTGCCTC ATGATGATAA ACATGTTGA CAAGACCAAG 360
TCAGGCCGCA TCGATGCTA CGGCTTCTCA GCCCTGTGGA AATTCATCCA GCAGTGGAA 420
AACCTCTTCC AGCAGTATGA CCGGGACCGC TCGGGCTCCA TTAGCTACAC AGAGCTGCAG 480
CAAGCTCTGT CCCAAATGGG CTACAACCTG AGCCCCAGT TCACCCAGCT TCTGGTCTCC 540
CGCTACTGCC CACGCTCTGC CAATCCTGCC ATGCAGCTTG ACCGCTTCAT CCAGGTGTGC 600
ACCCAGCTGC AGGTGCTGAC AGAGGCCTTC CGGGAGAAGG ACACAGCTGT ACAAGGCAAC 660
ATCCGGCTCA GCTTCGAGGA CTTTCGTACC ATGACAGCTT CTCGGATGCT ATGACCCAAC 720
CATCTGTGGA GAGTGGAGTG CACCAGGGAC CTTTCCTGGC TTCTTAGAGT GAGAGAAGTA 780
TGTGGACATC TCTTCTTTTC CTGTCCCTCT AGAAGAACAT TCTCCCTTGC TTGATGCAAC 840
ACTGTTCCAA AAGAGGGTGG AGAGTCTCTG ATCATAGCCA CCAATAGTG AGGACCGGGG 900
CTGAGGCCAC ACAGATAGGG GCCTGATGGA GGAGAGGATA GAAGTTGAAT GTCCTGATGG 960
CCATGAGCAG TTGAGTGCCA CAGCCTGGCA CCAGGAGCAG GTCCCTGTAA TGGAGTTAGT1020
TGCCAGCTAG CTGAGCTCCA CCCTGATGCC AGTGGTGAGT GTTCATCGCG CTGTTACCGT1080
TAGTACCTGT GTTCCCTCAG CAGGCCATCC TGTCAAACGA GCCCATTTTC TCCAAAGTGG1140
AATCTGACCA AGCATGAGAG AGATCTGTCT ATGGGACCAAG TGGCTTGGAT TCTGCCACAC1200
CCATAAATCC TTGTGTGTGA ACTTCTAGCT GCCTGGGGCT GGGCCTGGCT AGACAAATCT1260
GCTCCCTGGG CATCTTTGGC CAGGCTCTG CCCTCTGCAG CTGGGACCCC TCACCTGGCT1320
GCCATGCTCT GCTCGGCTTC AGTCTCCAGG AGACAGTGGT CACCTCTCCC TGCCATACT1380
TTTTTTAATT TGCATTTTTT TTCATTGGG GCCAAAAGTC CAGTGAAATT GTAAGCTTCA1440
ATAAAAGGAT GAAACTCTGG AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA1500
AA

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1502

(2) INFORMATION ON SEQ ID NO. 226:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 1892 base pairs
 (B) TYPE: Nucleic acid
 (C) STRAND: individual
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 (A) ORGANISM: HUMAN
 (C) ORGAN:
- (vii) OTHER ORIGIN:
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 226:

CATAATTTCG TTTAGAGTCA TTTTCCAGC AATGTTTAAA TTACTTTCTC ATTCTTTTAG 60
 TGTATTCAAC ATTGCTGCC TCTTCCTGCA GTTGATGTAA TTGCTTTGTT TGCAATAGCA 120
 CAAGCTGCAT TATTCAGTC AGGACTGTGA TAACTTGCTG CCAGCCCCAC TCAACTTTCA 180
 GTTGGCTCTG TGTCACTTTT CCACTCAGTG AGCTCATCAC AGCCTAGAGT TAAGTAAAGT CAATTCACAG 300
 CCTCCCTTGA AGTGCTATA AGTGCATCAC AGCCTAGAGT TAAGTAAAGT CAATTCACAG 300
 AAGCACAAAT TTGCCCTTTG CGAGACATTG TTGCCTCTAT CTAGTCTCTAC AAGTAGGGTT 360
 TTGCATACCTG TGTTTGCCCC TAGGGTTGTC AGTGCATCAG AAATACTTCT AAATAGTGGT 420
 AAAAATGCAC ATGGTTAAATG CACATGTATC TTTTAAATCA TTAGGATATC CCTCACCTGT 480
 TCCTGATGAA TAAAAAGTGT GTTAAAGACC AAAATTCCTG GCATAATAAT CAGCTACATA 540
 CAAATCAGAT ATAGTTTAAAT CTTTTTTAAAT GAAAAAATAA TCATGTTTAA AATGGCAAAA 600
 GCCCATCTTA TACATCTTTA TATAGCTGCA AAAAATTTAT ATCTGTACAG ATCTAACACT 660
 ACGCACTCA GATATCACTT TATTGAAGCA TGCAAGTAAA GCACCTTTTTC TAATTTATAT 720
 AGAGGTATCT AATTAACACA GCACATTGTA CTAATGACTA GGAGTAGCAG CTTTTTCTTC 780
 TCTCCCTCTA TGAATCTTGA TAATGTCCTT TTTTCTGTAA GTTTTTGAGA GCGCAATGGC 840
 AATTAGGAGT GCAGCAGGGT CTGTTTGGGT CAAATCTTGA ATTTCTGTGT TGCACCTAG 900
 TGCATGATCT TTGGGAATGT CTTGCTCTTG CATGGGGCTC ATAGAGATGT GTGCAGACTT 960
 GCCTATTGTG GTTAGTGTGT ATCAGGAACA CACACACAGG TGTTCTGACC AGCTCAGGCT1020
 TGCCACAGTG AGCAACTCTG TGGCTAGCAA AAGAGAAGTT TATTTGTGCC CAGCCATTGG1080
 TCACCTTGGG TGATGCACCA GATAGCAGGC AGATGTTGGT TCATTGGCCT TCGTCTCTT1140
 TCCTCCTAAA ATAATATTGG CTTTACCATC TTAACCTCAG TGTGGGTTTT TTGTTGGGTT1200
 TTGTTTGTGT TTTGGCATGA ATTGTCATCT TTGGTGTTTT TTTAACCCCC AGCCCCCTCA1260
 AAAAATAAGG CCTCCAGGTA TCAAGATCTC ATATTAGGAT TTTCTGTCTT TAATTTTTT1320
 AGCAAAATCT GGAATATTGT AAGCATATT TAGATTTTAT ATACTATCTG AAATGTGATT1380
 TGTTAAGATT CTTAAATTTG GGCCTCTTAG AATAATTTTG AATGAGATCT ACCGACTCAC1440
 TTGTGAGAAAT ATTTTTCACA GATTATCTTT GGGCCTTTTC ATTAGAAGC CAGATTGTGA AAGCTCACAG1500
 TCCCCCTGTT GGTACATTTG GTTACCTCAT TTTGCCGTTT CAGATTGTGA AAGCTCACAG1560
 GGGTGTTTTT TGGAAATATT TGCTGAGTCA TTTTCTCAAA TCATATTCCA TTGTATCAGT1620
 TAACATATAG TTTTAAATGT ATGATATTATA AATACTCTGA ACCAAATCAT TTGAAGGCTT1680
 GATAAATTTT TAACAAAGTT TGTACATTTT TTATGAAAGT TACTAGTAAT GCTTTACTAA1740
 TGAGTGCAAT GAATTTTTTAT TTTTAAATCCC TGTGCCCAAT TTGGAGTTGT AGAGGGTTGT1800
 TGGTAATAAA TGTATGATGT ACACCTTAAA AAAAAAATAA AAAAAAATAA AAAAAAATAA1860
 AAAAAAATAA AAAAAAATAA AAAAAAATAA AA 1892

(2) INFORMATION ON SEQ ID NO. 227:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 1522 base pairs
 (B) TYPE: Nucleic acid
 (C) STRAND: individual
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 (A) ORGANISM: HUMAN
 (C) ORGAN:
- (vii) OTHER ORIGIN:
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 227:

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CAGGAGTGC GACACGCGGG TGCCTGTAGT GGGTGAATT GGGGTCTGCA CTTGCCCTC 60
CGCCCCCAGG TGGGAGTCAC CTGGAGCGTG AAGGGACGTG TCTCATCCCC AGTGTGTCGG 120
ACCTGGGAGA CACAGCCGCA GGCAGCCCCC TTCTCATGCA TGGACCTCAC CTACGTCAGC 180
CTGCTACTCC AGGAGTTCGG CTTTCCCAGG AGCAAAGTGC TGAAGCTCAC TCGGAAAATT 240
GACAATGTTG AGACCAGCTG GGCCTCTGGG GCCATTTTTC ATTACATCGA CTCCTGTAAC 300
AGACAGAAGA GTCCAGCCTC ATAGTGGCCG AGCCATCCCT GTCCCCGTCA GCAGTGTCTG 360
TGTGTCTGCA TAAACCCTCC TGTCTTGAGC GTGACTTCAT CCTGAGGAGC CACAGCACAG 420
GCCATCAGCC TCTTCCAGTC ACATCTGGCC AGAGGGCTGT CTGGACCTGG GCCCTGCTCA 540
GCCGTGCTGG CACTTTCTGC AACTTGCTC TGGGACTTGC AGAAGGCTGT GTGCTGCCCT 480
GGCATCAGCC TCTTCCAGTC ACATCTGGCC AGAGGGCTGT CTGGACCTGG GCCCTGCTCA 540
ATGCCACCTG TCTGCCCTGG CTCCAAGTGG GCAGGACCCG GACAGAACCA CAGGCACACA 600
CTGAGGGGGG AGTGTGGCTC CCTGCCCTGC CCATCCCCAT GCCCGCTCCG CGGGGCTGTG 660
GCTGCTGCTG TGCATGTCCC TGCATGGGA GTCTTGCTCT CCAGCCTGTC AGTTTCTCTC 720
CCAGGGCAGA GCTCCCCCTC CTGCNAGAGT CTGGGAGGCG GTGCAGGCTG TCCTGGCTGC 780
TCTGGGGAAG CCGAGGGACA GCCATAACAC CCCCGGGACA GTAGTCTGCG CGGCACCCAC 840
TGGGAACCTC GGACTTGAGT GTGTTTGCTT CTTCCTTGGG TATGAATGTG TGAGTTACAC 900
CAGAGGCTCT CTCTCCTCAC ACATTGTGTG GTTTGGGGTT AATGATGGAG GGAGACACCT 960
CCTCATAGAC GGCAGGTGCC CACCTTTCAG GGAGTCTCCC AGCATGGGCG GATGCCGGGC1020
ATGAGCTGCT GTAACTATT TGTGGCTGTG TCGCTTGAGT GACGCTCTGT TCGTGTGGGT1080
GCCAAGTGCT TGTGTAGAAA CTGTGTTCTG AGCCCCCTTT TCTGGACACC AACTGTGTCC1140
TGTGAATGTA TCCTACTGTG GAGCTGTTCC CGCCTAGCCA GGGCCATGTC TTAGGTGCAG1200
CTGTGCCACG GGTCAAGCTG GCCACAGTCC CAGAACCAAG CTCTCGGTGT CTCTGGGCCAC1260
CATCCGCCCA CCTCGGGCTG ACCCCACCTC CTCCATGGAC AGTGTGAGCC CCGGGCCGTG1320
CATCCTGTCT AGTGTGCGGT CAGTGTGCGG GCTGAGCCCC TTAGAGCTGCT TCAGTGAATG1380
TACAGTGCCC GGCACGAGCT GAACCTCATG TGTTCCTACT CCAATAAAAG GTTGACAGGG1440
AAAAAAAATA AAAAAAAACT CGAGCGGAAC GAGCTCACTT TCTTCTAGCT GAGCTTTAAA1500
ACATTAGAGC TTAATTTTTC AG 1522

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(2) INFORMATION ON SEQ ID NO. 228:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 2016 base pairs
 (B) TYPE: Nucleic acid
 (C) STRAND: individual
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 (A) ORGANISM: HUMAN
 (C) ORGAN:
- (vii) OTHER ORIGIN:
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 228:

GAGAAATG AGGCCCTTGG GGAAGGGGCA GGGTGGGAGG ATTTCTTCTC CACACAGACC 60
 TTAACCTTCC AATCTATTCT GCAGATGAAG AATGCCGACT ACTTCTCCAA CTATGTCACA 120
 GAGGACTTTA CCAGCTTACAT TAACAGGAAG CGGAAAAACA ATTGCCATGG CAACCCACATT 180
 GAGATGCAGG CCATGGCAGA GATGTACAAC CGTCCTGTGG AGGTGTACCA GTACAGCACA 240
 GAACCCCATC ACACATTCCA TGGGATACAT CAAAACGAGG ACGAACCCAT TCGTGTTAGC 300
 TACCATTGGA ATATCCACTA TAATTTCAGT GTGAATCCTA ACAAGGCCAC CATTGGTGTG 360
 GGGCTGGGCC TGCCATCATT CAAACCAGGG TTTGCAGAGC AGTCTCTGAT GAAGAATGCC 420
 ATAAAAACAT CGCGAGGAGT ATGGATTGAA CAGCAGATGC TAGAAGACAA GAAACGGGCC 480
 ACAGACTGGG AGGCCACAAA TGAAGCCATC GAGGAGCAGG TGGCTCGGGA ATCCTACCTG 540
 CAGTGGTTGC GGGATCAGGA GAAACAGGCT CGCCAGGTCC GAGGCCCCAG CCAGCCCCGG 600
 AAAGCCAGCG CCACATGCAG TTCGGCCACA GCAGCAGCCT CCAGTGGCCT GGAGGAGTGG 660
 ACTAGCCGGT CCCCAGGCCA GGGAGTTCAG CCTCGTCACC TGAGCACCTT GAGCTGCATG 720
 CTGAATTGGG CATTGAAGCCC CCTTCCCCAG GCACTGTTTT AGCTCTTGCC AAACCTCCTT 780
 CGCCCTGTGC GCCAGGTACA AGCAGTCAGT TCTCGGCAGG GGCCGACCGG GCAACTTCCC 840
 CCTTGTGTGC CCTCTACCTT GCTTTGGAGT GCGCGGCCCT CATTGAGCAG ATGTCCCCCT 900
 CTGCTTTTGG TCTGAATGAC TGGGATGATG ATGAGATCCT AGCTTCGGTG CTGGCAGTGT 960
 CCCAACAGGA ATACCTAGAC AGTATGAAGA AAAACAAAGT GCACAGAGAC CCGCCCCCAG 1020
 ACAAGAGTTG ATGGAGACCC AGGGATTGGA CACCATCTCC CAACCCCAGT ACTCTGTGCT 1080
 TCCGGTGCCA CCTCACCTTC TTTGGCTTCT TCCCTCTTGT CTCTTCTGCT 1140
 TCCCCCTCTT TTCCCTCTCT CTTCACTTCCC TCTGGCTAGC CCACCCCTGC ACTCTCTCTC 1200
 ATTGCCCGCT GCACTATCAC CTGTCTCTCT GCCAGCTGAT GTGCCCTGTT GCCCCCCACC 1260
 CCATCCCCGA CAGAACCTAC CTGTGATTC ACAGGGGAGT CGGGCAAGGG TCGCGAAGAT 1320
 AGACRAGAGG CACACAGAGA CAGACCAACT GGCAGCCAGG GCAGCCACGA GGAGCAGAC 1380
 ATTACAGACG AGGAAAGTCT CCTGCCCCCT CATTCCTTCC AAGATGAGAA AAACCTGCCG 1440
 CCACCCCCCG ACACGTGATG CAGGGAGGTT GGAGGAAGAA GTGGGAAATT TCCCTTCCCA 1500
 GTACCCCCAA GAAGCTGTGA GCCTTCAATG TTGAATTTT TCTTTATTAA AATTACTTTT 1560
 ATCTTATAAA ATCAACTAAT CAAAAATGAT ATAGACGACA GCACTGGGTC TGTGAAGGTG 1620
 GCATCTTTCT GGGCAGGCAG CCATGGGGC ATGGAGGAGG GTGCRAAGAT ATGGGTTGCT 1680
 GTCTTCTGCG CTCAGCTGAC ATGGAGGCCG GCCCAGGGTC TAGGGTGTGC ACTGGGCAAG 1740
 GGCAGGGCGC CAGGTGTGAC GCGCGCTTGG ACAATGAACC CTTGACTTTG CTGCATTCTT 1800
 TTTGCTTCCA CCACCACTAG CTTCTTTTGA ATCTTGGGGT GGGGGTCATC TTTGGGGATT 1860

ATGGCTGCCA CCCGGGATTT GAGTGTAGGG AGTGTGGGAG CAGCCTTGGC AGAAGGGGCA 1920
 CCCGTGCCCT GCAGGTGTGG ACAAGATCCG CCATCTGTAA TGTCTTGGC ACAATAAAAC 1980
 CAATGTCTAG TTTCAAAAAA AAAAAAAAAA AAAGAC 2016

(2) INFORMATION ON SEQ ID NO. 229:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 765 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 229:

CCGGATTCCG	CCCGGCCCGC	TGCGATCCGG	TTCCGCTCCC	CACAACCCGC	TCTGTGGCGG	60
GGCTTCCGGT	CGGGAGGGTC	CGCCAGCTCT	GCGCTCCTTT	GCTGGGTCCA	GACACCGGTT	120
CCGTTGCAAA	CATTTTAAAA	GGGCTGGTTA	TTCTTCCTGA	AATGAGTTTG	GTGATTAGAA	180
ATCTGCAGCG	AGTCATCCCC	ATCAGGAGAG	CGCCACTTCG	CAGTAAGATC	GAGATTGTAA	240
GGAGGATTTT	AGGAGTGCAG	AAATTTGACC	TGGGGATCAT	CTGTGTTGAC	AACAAGAATA	300
TTCAGCACAT	TAATAGAATC	TACAGAGATA	GAAATGTCCC	AACCGATGTG	CTTCTTTTC	360
CATTTCATGA	GCATCTGAAA	GCAGGTGAAT	TTCCCCAGCC	TGATTTTCCA	GATGACTACA	420
ATTTGGGAGA	CATTTTCCCTA	GGAGTGGAGT	ATATCTTCCA	TCAGTGTAAG	GAAATGAAG	480
ATTACAATGA	CGTCCTGACT	GTGACGGCCA	CCCACGGACT	CTGTCACTTG	CTGGGATTCA	540
CACACGGCAG	GGAGGCAGAG	TGGCAGCAGA	TGTTCCAGAA	GGAGAAGGCG	GTGCTGGACG	600
AGCTGGGCGG	ACGCACGGGG	ACCCGGCTGC	AAGCCCTGAC	CCGGGGCCTC	TTCGGAGGGA	660
GCTGAGGGCC	GCGTTCCTTC	TGAAAGCGGG	ACGCGGGAGG	GGTGGAGGCT	GCGGGGAGCC	720
GGGGTCGCAC	ACAAATAAAT	AACGAATGAA	CGTAAAAAAA	AAAAA		765

(2) INFORMATION ON SEQ ID NO. 230:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1611 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 230:

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CTGCTTGGCG CGACGCTCTA GCGGTTACCG CTGCGGGCTG GCTGGACCGT AGTGGGGCTG 60
CGCGGCTGCC ACGGAGCTAG AGGGGTAA AACTAATATT TATATGACAG AAGAAAAAGA 120
TGTCATTCCG TAAAGTAAAC ATCATCATCT TGTCCTGGC TGTTGCTCTC TTCTTACTGG 180
TTTTGCACCA TAACCTCCCTC AGCTTGAGCA GTTTGTTAAG GAATGAGGTT ACAGATTTCAG 240
GAATTGTAGG GCCTCAACCT ATAGACTTTG TCCCAATGC TCTCCGACAT GCAGTAGATG 300
GGAGACAAGA GGAGATTCCCT GTGGTCATCG CTGCATCTGA AGACAGGCTT GGGGGGGCCA 360
TTGCAGCTAT AAACAGCATT CAGCACAAAC CTGCTCCAA TGTGATTTTC TACATTGTTA 420
CTCTCAACAA TACAGCAGAC CATCTCCGGT CCTGGCTCAA CAGTGATTCC CTGAAAAGCA 480
TCAGATACAA AATTGTCAAT TTTGACCCTA AACTTTTGGA AGGAAAAGTA AAGGAGGATC 540
CTGACCCAGG GGAATCCATG AAACCTTTAA CCTTTGCAAG GTTCTACTTG CCAATTCTGG 600
TTCCCGCGC AAAGAAGGCC ATATACATGG ATGATGATGT AATTGTGCAA GGTGATATTC 660
TTGCCCTTTA CAATACAGCA CTGAAGCCAG GACATGCAGC TGCATTTTCA GAAGATTGTG 720
ATTCAGCCTC TACTAAAGTT GTCATCCGTG GAGCAGGAAA CCAGTACAAT TACATTGGCT 780
ATCTTGACTA TAAAAAGGAA AGAATTGCTA AGCTTTCCAT GAAAGCCAGC ACTTGCTCAT 840
TTAATCCTGG AGTTTTTGT TGCAAACCTGA CGGAATGGA ACGACAGAAT ATAACATAAC 900
AACTGGAAAA ATGGATGAAA CTCAATGTAG AAGAGGGACT GTATAGCAGA ACCCTGGCTG 960
GTAGCATCAC AACACCTCCT CTGCTTATCG TATTTTATCA ACAGCACTCT ACCATCGCAT1020
CTATGTGGAA TGTCCGCCAC CTTGGTTCCA GTGCTGGAAA ACGATATTCA CCTCAGTTTG1080
TAAAGGCTGC CAAGTTACTC CATTGGAATG GACATTGAA GCCATGGGGA AGGACTGCCTT1140
CATATACTGA TGTTTGGGAA AAATGGTATA TTCCAGACCC AACAGGCAAA TTCAACCTAA1200
TCCGAAGATA TACCAGATC TCAAACATAA AGTGAAACAG AATTTGAACT GTAAGCAAGC1260
ATTTCTCAGG AAGTCTCGGA AGATAGCATG CGTGGGAAGT AACAGTTGCT AGGCTTCAAT1320
GCCTATCGGT AGCAAGCCAT GGAAAAAGAT GTGTCAGCTA GGTAAAGATG ACAAACCTGCC1380
CTGTCTGGCA GTCAGCTTCC CAGACAGACT ATAGACTATA AATATGTCTC CATCTGCCTT1440
ACCAAGTGT TCTTACTAC AATGCTGAAT GACTGGAAG AGAAGTACT ATGGCTAGTT1500
CAGCTAGCTG GTACAGATAA TTCAAAACTG CTGTTGTTT TAATTTTGTA ACCTGTGGCC1560
TGATCTGTAA ATAAACTTA CATTTTTC AAATAAAAAA AAAAAAAGA T 1611

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(2) INFORMATION ON SEQ ID NO. 231:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 1473 base pairs
 (B) TYPE: Nucleic acid
 (C) STRAND: individual
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 (A) ORGANISM: HUMAN
 (C) ORGAN:
- (vii) OTHER ORIGIN:
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 231:

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GGTGTGGTCC TCAGGGGGCT GTAGGCTGGG AGGTATGGCT TCAGGTGCCA AGTTGGCGGG 60
AACGGCAGCG AGGAGGCCTG GGGGGCACTT CGGGCGCCGC AACAGCAGGT ATCCCAATAG 120
CTCCAAACCC TATCACGACA GCCATTTGTC TCTTTCCCTT TTCCTTGTC CTTCCTTTTG 180
GGGGTGGGGG AGGAACACAC GGAGCCAAAG GTACTGTGAA GTTCCTAAAC ATGCTCTCTC 240
CACTCTTTGT CTAACACTTTG TAACGTAGAT GCAGCTGACT TTGCCTGTAG CCTCATAGAA 300
CCCATCCCAT GGCTGCAGTG GAAGCTTGCG GTGGCTCTCC AGTGACCAGA GGCATAGTGA 360
GGTCCCAGGG AGGCTCCCTC TGTCTTGCAA CAGTATTGTT TGATCTTTTT CTATGTGCCT 420
ATTGTACAAA CAGAGTCCGG CAGCGTCTTC TCTTGAGGGA GCAATTTGGA GAAGAGCTGG 480
AACCCAGACT CGCGCCCTGG ATGCCATCCT TTATCATCCA CAGCAATCCC ATCTGGTTGG 540
GAGCACTGCT CTGGGTCTCA CACTGCCCTT CCTCTATCCT AGGGAGCCTG AGGCCAGGG 600
GTGGAAGAGT CCAAGTTGCG GTGGGGGGTA GTGAACCGTG CAGGATAATG AAAGCAACTT 660
GCTTTGGAAA TGACCTACCG CTACCCGTTG TCTGAGACTG AGATTATCTC AGACTGTCTT 720
CTGGCTTCTG CCAAAACACT CCCTTAACAG AAAGCACCGA GGGGATGGGG GTAGGGGGGT 780
TGGGGAGAGT GAGGCTTGAG TGTGAAGGAA GTCTCATATA TGCAGAGCTG AAATCTCCCT 840
CTTTGTATGT CCACACTTTT GTCTTGTCT CTAGACTGAT TCTTGCTATT CCAAACTCTC 900
TTCCACCTTG ACAGCCCTTC AGATATTCTA CACTCCTCTC CAGCATCCTC CACTTCCCCC 960
ATCTCTCCAA GCTGAACCTG GTTCACAGGG TGGGATTGTG TATGTGCATG CAGGAGGTGG1020
GGTGGGACAG TGCCCTGGGC TGGAATCCCC CTTAGTTCTA AGTGCTCTCT TGCCCGCAGG1080
TTGAGAGAGT GTGCCCGAGA GTGAACAACC AGCCCTACCT CTGTGAGAGT TGTGCTGCTT 1140
GCGGGGAGAC TGCGCTGCTG ACCTACTACT ATGAGCTCTG GTGGTCTCTG CTGCTCTGGA1200
CTGTCTCAT CTCTTTTACG TGCTGTTGCG CCTTCCGCCA CCGACAGAGT AAACTCAGGC1260
TGCAACAACA GCAGCGGCAG GTGGAATACA ACTTGTGGC CTATCATGGG GCATGCCATG1320
GGGCTGGTCC TTTCCCTACC GGTTCACCTG TTAGCCTTCG CTTCCTCAGC ACCTTCAAGC1380
CCCCAGCCTA CAGAGATGTG GTTCACCGCC CAGGCACAAC GAGCCCCCCC TTATACTGTG1440
GCCCCAAGCA GCCCCCTGAG GTTGTTTCAA GTG 1473

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(2) INFORMATION ON SEQ ID NO. 232:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 2503 base pairs
 (B) TYPE: Nucleic acid
 (C) STRAND: individual
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 (A) ORGANISM: HUMAN
 (C) ORGAN:
- (vii) OTHER ORIGIN:
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 232:

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GAAACATGCA ACTGAACAGG AAAAAACTGA AGAGGGATTA GGCCCTAATG TAAAGGCAT 60
TGTCACCATG TTGATGCTGA TGCTATTGAT GATGTTTGGC GTCCACTGTA CCTGGGTCAC 120
AAAGCAATGCC TACTCTAGTC CAAGTGTAGT CCTGGCCTCA TACAATCATG ATGGCACCAG 180
GAATATCTTA GATGATTTTA GAGAAGCCTTA CTTTGGCTA AGGCAAAATA CAGATGAACA 240
TGCACGAGTA ATGTCTTGGT GGGATTATGG CTATCAGATA GCTGGAATGG CTAATAGAAC 300
TACGTTGGTG GATAATAACA CTGGAATAA CAGCCACATA GCACGTGGTG GAAAAGGTAT 360
GTCTTCTAAT GAAACAGCAG CCTATAAAAT CATGAGGACT CTAGATGTAG ATTATGTTTT 420
GGTTATTTTT GGAGGGGTTA TTGGCTATTC TGGTGTATGAT ATCAACAAAT TTCTCTGGAT 480
GGTTAGGATA GCTGAAGGAG AACATCCCAA AGACATTCCG GAAAGTGACT ATTTTACCCC 540
ACAGGGAGAA TTCGCTAGAT ACAAAGCAGG ATCCCTTACT TTGTTGAATT GCCTTATGTA 600
TAAATGTCA TACTACAGT TTGGAGAAAT GCAGCTGGAT TTTCTGACAC CCCCAGGTTT 660
TGACCGAACA CGTAATGCTG AGATTGGAAA TAAGGACATT AAATTCAAAC ATTTGGGAAG 720
AGCCTTTACA TCAGAACACT GGCTTGTTAG GATATATAAA GTAAAGACAC CTGATAACAG 780
GGAGACATTA GATCACAAC CTGAGTGCAC CAACATTTC CCAAAACAGA AGTATTTGTC 840
AAAGAGACT ACCAAAGGA AGCGTGGCTA CATTAAAAAT AAGCTGGTTT TTAAGAAAGG 900
CAAGAAAAATA TCTAAGAAGA CTGTTTAAAT GCACGTGTTCT GGTTCCTAAC TTGAAGCAGT 960
TGTCCTTGTG AGAACGGGTC TTGCTCTTTA GCTCATGTG TGTTCACAG CAAAGAGGGT1020
ACAGAACCAT CACTGGTCCA GGTTAATGTA CAAAATTTTC TGCCATGCCC TGGTAAAAA1080
AATAAAATTT GCTGTGTGAG AACAGCTGTT TTGATTTCT ATGTGGAAGC AAGACAGAGC1140
ACTGCTGTA ATGTCTAGCA GCAGATTTTT TTTTATTG TACATATTAT CCTTCAAAT1200
TGAGAAATTT GACTAAGCTG ACCAAGAAGC CCTCTAATT GGTCCTGGC ACATGCATAC1260
TTGTCAATGT TTTTATCTTT TTACAAGACC TGCATTTTAT TTGTAATTACC CGAATAGCA1320
TATGTAAAT ACAAGTGATG AATGTGATG AGAGCTTCTT GAACCGGTAA ACTAGTACAG1380
GTCTGAGAAA GACATATTAG AAGAATCATT ATACTTCCTT GAATTATATT TATTTTCATG1440
TTTCTCTAAT GCAAAAGATG TTTTATCAA TGTATATTTT CTGTTGCTTA CTGTTTGCTC1500
TGAGAAGAG CTGCTGTTTC AAGATGGGAC CTCTGAGTAG CTAATTGATT CAAGTAGTTT1560
TTTTATGTTG ACACATTATT ATGCTGTGTA GCAGTCGTTT TCACCAAGGTA-CTTACAGAGC1620
AGATTTTCATA CATCATTTCAT TCAAGGGCTA AATTATATT TTTTGGAAAT CATGGCAACT1680
ACACAGGATG TTGCTTACCA GGACGGAGTT TTGGTATCTT AGTACTGAAG TTAGCATATT1740
GTTTACATGC AAAGATTTAA GGAAAAAACC CTTAAAGTGC ACAGGTTATCC AAAGTTCATT1800
TTCTGTGACT CATCAAAGTG ACAAAGACT TGTAAACA CTGCTGGGAC TTTTTCATT1860
TTACAACAGT TCATCCATTC ACAATGATTT TGTTCTCTGC TCCATATTTT TTAATCCCTT1920

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AAGCATTGTA TGAAACACTC TTTAGTGCTA TATGCATTTT CTTACTTTTG TTA AAAATGT1980
 GACAATTGTC AAAAAATGCA CTAAAATGTA AATGGAGATT GAACAAGTTC ACTTTCCAGC2040
 TTTATAGGCAA CTTTATACAG ACTTGAACAT TTTCTCCAGT TGTTTAGTAA AAGTGAAAGA2100
 GAAAGGGTTT TTCTGCCAC AGGATATAAC TTTTTTTTAT ATAACAAGCA TAACACACCA2160
 CTGCTTTTG TGGAAAAGTG CAGAATAGTA TGTACCTTTT ATGAAGAAAA ATGTAATTTA2220
 CAATATTCAG TGAGAATGTT ACTGCTGATT TTCTTTTCCA AGGTGTAGAA TATTCTTTGA2280
 TTTTAGAAT TCATTTTTGA CCCAGATGAT GGTTCCTTTA CAGAACAAATA AATTGGCTGA2340
 ACATTTTTCAC AAATAGAGTG TAACGAAGTC TGGATTTCTG ATACCTTGTG ATTTGGGGGA2400

TTTTATTTTA CTTTGTGCT TAAAAATTCA ATGCAGAGAA GTTGTGACT GTAGGGGAAA2460
 TAAAGTTAAT TCAAAATTTG AAAAAAAGTCG ACG 2503

(2) INFORMATION ON SEQ ID NO. 233:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1756 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 233:

AAGCAACCTC	GTTTATGTCT	TATCTTTGCA	TTTTCTTGTA	TTCAGCTATT	TTCTTAAAGG	60
AAGGCCCAGG	TCTGTATTAT	CCTACTGCCA	CATAGGAAAT	AAAAATGAGTA	CTCACAGCCT	120
TGCGCCATAAT	CACCTGAACAC	AGCTTTTATG	AATGTTTTAC	ACAAGAACAG	GATATTGGCA	180
ACTCAACTGT	TAAGCCCTTC	TGTGATTATT	CTTCCTTGAG	ATCACTCTGA	TGTCACCAGT	240
GTAATTTGAG	CCTGGAAGCTT	TTGTTCCAC	TTTAAATAGC	AGTCCCAGAA	TGATTTCACT	300
ACAGACTCTC	TGGAAAAGCCT	GGGAGCTGAA	TTCCGGAAAG	TCCCCACATC	GATGAAAGCA	360
AAGCGAAGCA	CCAAGCCATC	ATCATGTCCA	CGTCGCTACG	AGTCAGCCCA	TCCATCCATG	420
GCTACCACCT	CGACACAGCC	TCTCGTAAGA	AAGCCGTGGG	CAACATCTTT	GAACACACAG	480
ACCAAGAATC	ACTAGAAAGG	CTCTTCAGAA	ACTCTGGAGA	CAAGAAAGCA	GAGGAGAGAG	540
CCAAGATCAT	TTTTGCCATA	GATCAAGATG	TGGAGGAGAA	AACGCGTGCC	CTGATGGCCT	600
TGAAGAAGAG	GACAAAAGAC	AAGCTTTTCC	AGTTTCTGAA	ACTGCGGAAA	TATTCATCA	660
AAGTTCACTG	AAGAGAAGAG	GATGGATAAG	GACGTTATCC	AAGAATGGAC	ATTCAAAGAC	720
CAAGTGAGTT	TGTGAGATT	TAACAGATGC	AGCATTTTGC	TGCTACCTTA	CAAGCTTTCT	780
TTCTGTCAGG	ACTCCAGAGG	CTGGAAAGGG	ACCGGAGCTG	GAAAGGGACC	AGGACTGAAC	840
AGACTGGTTA	CAAAGACTCC	AAACAATTTT	ATGCCCTGTG	CTGTTACAGA	GGAGAACAAA	900
ATGCTTTTCA	CAAGGATTTG	AAAACCTCTT	CGTCCCTGCA	GGAAAGGATT	GATGCTGATA	960
GAAGAGCCTG	GACAGATGTA	ATGAGAACTA	AAGAAAACAG	ATGGCTGGAG	ATGACATTTA	1020
TCCAGGGTCA	CTTTGTTCAG	CCCTAGGACT	TAAATCGAAG	TTGAACTTTT	TTTTTTTTTT	1080

AACCAAATAG ATAGGGGAGG GGAGGAGGGA GAGGGAGGAC AGGGAGAGAA AATACCATGC1140
 ATAAATTGTT TACTGAATTT TTATATCTGA GTGTTCAAAA TATTTCCAAG CCTGAGTATT1200
 GTCTATTGGT ATAGATTTTT AGAAATCAAT AATTGATTAT TTATTTCAC TTATTACAAT1260
 GCCTGAAAAA GTGCACCACA TGGATGTTAA GTAGAAATTC AAGAAAAGTAA GATGTCCTCA1320
 GCAACTCAGT AAAACCTTAC GCCACCTTTT GGTTTGTAAA AGGTTTTTTA TACATTTCAA1380
 ACAGGTTGCA CAAAGTTTAA AATAATGGGG TCTTTTATAA ATCCAAAGTA CTGTGAAAAC1440
 ATTTTACATA TTTTATAAAT CTCTGACTA ATGCTAAAAC GTAATCTAAT TAAATTTCA1500

ACAGTTACTG CAGTAAGCAT TAGGAAGTGA ATATGATATA CAAATAGTT TATAAGACT1560
 CTATAGTTTC TATAATTTAT TTTACTGGCA AATGTCTATG AACAATAATA AATTATTGTA1620
 AACTTTGTGA AAAATAGTCT GTGATGCTTG GTCTCAAAGG AAAAAATAAG ATGGTAAATG1680
 TTGATATTTA CAAACTTTTC TAAAGATGTG TCTCTAACAA TAAAAGTTAA TTTTAGAGTA1740
 AAAAAACGG CTCGAG 1756

(2) INFORMATION ON SEQ ID NO. 234:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1286 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 234:

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GCCTAGGATC CCTGTGACCC TCAACATGAA GATGGTGATG CCCTCCTGTC AAGGCCCTTGA 60
TTGAGCATGA AATGAAGAAC GGGATCCCTG CCAATCGAAT CGTCCTGGGA GGCTTTTCAC 120
AGGGCGGGGC CCTGTCCTCT TACACGGCCC TCACCTGCCC CCACCCCTCTG GCTGGCATCG 180
TGGCGTTGAG CTGCTGGCTG CCTCTGCACC GGGCCTTCCC CCAGGCAGCT AATGGCAGTG 240
CCAAGGACCT GGCCTACTCT CAGTGCCATG GGGAGCTGGA CCCCATGGTG CCCGTACGGT 300
TTGGGGCCCT GACGGCTGAG AAGCTCCGGT CTGTTGTCAC ACCTGCCAGG GTCCAGTTCA 360
AGACATACCC GGGTGTCTAT CACAGCTCCT GTCTCTCAGG GATGGCAGCT GTGAAGGAAT 420
TTCTTGAGAA GCTGCTGCCT CCTGTCTAAC TAGTCGTGG CCCCAGTGCA GTACCCACAG 480
TCATGGGGGA CTCAGCAAGC AAGCGTGGCA CCATCTTGGA TCTGAGCCGG TCGAGCCCT 540
GTCCCCACCC TTCTTGACCT GTCCTTTTCC CACAGGCCTC TGGGGGCGAG TGGCAAGGCC 600
TGGCCGGGCC TTCTTCCCTG GCCTTAGCCA CCTGGCTCTG TCTGCAGCAG GGGCAGGCTG 660
CTTTCTTATC CATTTCCCTG GAGGCGGGCC CCCCTGGCAG CAGTATTGGA GGGGCTACAG 720
GCAGCTGGAG AAAGGGGGCC AGCCGCTGAC CCACTCACTC AGGACCTCAC TCACTAGCCC 780
CGCTTTGGGC CCCTCCTGT GACCTCAGGG TTTGGCCCAT GGGGCCCTCC CAGGCCCTG 840
CCCCAAGTGA TTCTGCCCCA ATAATCGTGT CTCCTGCCCT CACTCAGCTG CTCTCAGTC 900
ATGAATGTGG CCATGGCCCC GGGGTCCTCT TGCTGCTGTG GGCTCCCTGT CCCTGGGCAG 960
GAGTGCTGGT GAGGAGGTGG AGCCTTTTGA GGGGGGCCCT CCCTCAGCTG TTTCCCCACA1020
CTGGGGGGCT GGGCCCTGCC TCCCCGTTAC CCTCCTTCCC TGCAGGCTG GAGCCTGTAG1080
GGCTGGACTG AGGTTAGGT CTCCTCCAG CTGCTCACC CCCACTTTGT CCCCCTCTA1140
GAGCAGGGAG GCAGTGGGGG AGGAGTTGTG TCTCGTCTT TGTCTCCATG TGGTTTTTGG1200
GTGTTTTTCT TGTGTGTGCC TGGATTCCGA TAAATTTAA GAAATTGCTT CCTCAAAA1260
AAAAAAAAA AAAAAAAGT CGACGC 1286

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(2) INFORMATION ON SEQ ID NO. 235:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1230 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 235:

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ATTCCGCAAC GAGGTGAGAA AATCCCTTTT AAGGCCAAGG AAAGCTGAAT GCTAGCAGCC 60
AGGCCCTGTGG TACTTCCATG AGAAACCATA GCAGACAATG CCCTCCCAAG TACTGAAATC 120
ACACTGGGAAT CCCCCCTGTT GGGTTCATTT GATTGTTTAA CACAGGATGT GTTGTGTCAT 180
TCTGAAGTTT TTATTTGGGG CAGAAGTCTT TATGGAGATG TAAATGACAG CGTTTCTGGG 240
TTATGCATAA CTCTCTCACTG GTCAGAGACA CCGGTGTGTC AAGCATGGAT ATTGCATTGC 300
AAGACTTGAA TCTATAAAAA TTAGAATCAC ACAGTCAGTA CTACAAGCAA AACAGAGAAC 360
CTGAAAGAAG GTGCACAGAC TGTAAGAAAA AACCCAGTT TGTGATATTT CAGTGATTCC 420
AAAGAACATT CTAGGTTTTT TGTGTTTTT TTTGTTTTT GGGTTTTTTT TTTTACTGCA 480
GAAAAATTGGT GGTATTTTCA CATTCATAGT GTTTCATACC AATTTTCAGTA CCCACATTTA 540
ATGAGGAAAA AATGTTTTAC CAATGAAGGA GGAATTCCTA AATTAGCTGT AATGTTAGGT 600
TGGAGAAAAA TTGTATTTTA GGTATTTTC AAGGTACCAT CAAATCAGAT TTCGTTTTTT 660
TTGTTAAAAA AAATTTTTTT AATCAGTATT GTTTTTACAA GTAATATACT TTGAAACTCT 720
TGAACATAA CTCTCAAAAA CTCTAGAGGA CAGTCTGAGA ACACGTATTT CTATTGTTCT 780
AAATAAATAC ATGTTTTTGA ATAGTTCAT CATGAATTAT TGACTATGTC TTCATCAAAA 840
GTGTTAATCC CTCCTAGGGT CTCCTGGTGA GACCTTCAAG AGTTTGGTTT TTTCTCCCAG 900
GAAATTGGAA GGTAGAATGT TAAATTCATA GAACCTCTTT TATAATGGTG TACCTCAGCA 960
GCTGCCTTTC AATTATGCCC AAGTCCTTAC AGAGTTTATA CTTGAATAGT AAATATGTCT1020
TCTGAGTTTT ACAGTGTCTT AAACCTCAATG CACATTTTTT TTTCTCTCTT TTCCACCCCT1080
TCTTGTGTTG AGTTCATTAT ACCTGTCCTA TTACAGAACT GATTTCCCTC CTGGCTGTAC1140
ATGTTGGGGT GCTGGATTTT TTTCCGTGTC TTTAGTCTTC GGATACATGT TCTCTTCTTT1200
AGCTTGTGGT GAATACAGTA ATTTGCATTG

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1230

(2) INFORMATION ON SEQ ID NO. 236:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2328 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 236:

TGAGAGTTTA	GTTGTAGCAG	AGGGGCCACA	GACAGAAGCT	GTGGTGGTTT	TTACTTTGTG	60
CAAAAAGGCA	GTGAGTTTCG	TGAAGCCTGG	AAATTGGCCA	TGTGTCTTAA	GAGTGGCTGG	120
ACTTTGACAT	GTGGCTGTTT	GAATAAGAGA	AGGACAAAGG	GAGGAGAAAG	CACATGTGCT	180
CCAGTGAGTC	TTGCTCACTC	TGCTCTGCCA	GCAATTGATA	TATAACCGTG	ATTGTGTCTC	240
TGCTTTTCTT	CTGAAATGTA	GATAACTGCT	TTTTGACAAA	GAGAGCCTTC	CCTCTCCCCC	300
ACCCCTGTGT	TCTTGGGTAG	GAATGGGAAA	AGGGGCAACC	TACAAAGATT	GTTGGGGCAA	360
GGGAAGTCAC	AAGCTTTCCG	ATGGGCGGTG	GCTTTTCACA	AAACATTTAG	CTCATCTTAT	420
TCTCTCTTTG	TCTCTCTCC	CCTCCTGCCC	GCCCCGACCC	TGGAATTGCC	ACTCAGTTCC	480
TCGTGGGTGT	CACATATGTT	TGGAGAAATA	GAGGAGAGAA	AAGAGGGCCA	CGTAACTGAG	540
AGCTTACAGT	GCCAATGCCG	TTTGTGTTCT	GGCCAGAGTG	GAGTGCCGAG	CCTGACTCCC	600
AGGCCTGAG	ATTGTTGCCT	GGTTACCCAG	GAAGCTGCTG	TTCCGGCTGC	CCAGCCTTTC	660
TCGTAGCCAG	CGGATGCACA	GTCCGTGGCC	TTCTTCAGGC	TTATTGATGA	TGCTTTTTCG	720
AAATGTTGAA	TCATGGTTCT	GTTTCTAAGT	TGGATCTTTT	TTGTTTTCTC	CTTGCCACCC	780
TAATTGACA	TCAAAATTCT	TCTCTGTGCA	TTGGGCCCTG	GGTCATTCAA	ACCCAGGTCA	840
CCTCATTTCC	CTTCTCTGTT	CACACCTAAT	GTCTTGAAGA	GTAGGTAGCA	GCAGTGTGGG	900
CTGAACCTAG	GCCAGCTTGC	TTAGCGGGTC	ACCTCGCTGT	GAAGTCCTGG	CAGGTGTTGG	960
TAATGTGTGG	AAATGCAGTC	AGCAAGTTTG	CTGGGGAGTT	TGATAAAAAGT	ATAAAAACAAA	1020
ACAAAAAAG	CCTCGGTATA	ATTTTGTTC	ACGACTTCTT	CTGTAGCTTT	ACACCAGAAAG	1080
GAAAGAAATG	GCTACAGCAG	GTAGTGGAGG	AAGAGGGGGG	TGAGCAGGTT	TATTAATAA1140	
GCTTAGCGGT	AAGGCCATAA	AGGTCACCCC	TCCGCCCCCT	CTCCAAAAGA	AGGGCATGGG1200	
CACCCCCAGG	AGAGGATGGC	CCCCAAAACC	TTATTTTTAT	ACATGAGAGT	AAATAAACAT1260	
ATTTTTTTTA	CAAAAATAAC	TTCTGAATTT	ATCAGTGTTT	TGCCGTTAAA	AATATTCTCT1320	
TATAGTAAAT	TATTTATTGG	AAGATGACTT	TTTTAAAGCT	GCCGTTTGCC	TTGGCTTGGT1380	
TTCATACACT	GATTTATTTT	TCTATGCCAG	GCAGTAGAGT	CTCTCTGCC	CTGAGGAGCA1440	
GGCTACCCGC	ATCCCACTCA	GCCCTCCCT	ACCCTCAAG	ATTTGATGAA	AATTCCCAACC1500	
ATGAGGATGS	GTGCATCGGG	GAAGGGTGAG	AAGGAGAGCC	TGCCTGCTCA	GGGATCCAGG1560	
CTCGTAGAGT	CACTCCCTGC	CCGTCTCCCA	GAGATGCTTC	ACCAGCACCT	GCCTCTGAGA1620	
CCTCGCTCTC	TGTTCCAGCA	ACCCTGGTTG	GGGGGTGAGA	CTTGATACAC	TTTCAGGTTG1680	
GGAGTGGACC	CACCCCAGGG	CCTGCTGAGG	ACAGAGCAGC	CAGGCCGTCC	TGGCTCACTT1740	
TGCGATTGGC	ACTGGGTTGG	GGAGGAAGAG	AGCTGATGAG	TGTGGCTTCC	CTGAGCTGGG1800	
GTTCCTCTGC	TGTGCTAGTT	GTGAGCTGTC	CTCGGTGTTA	CCGAGGCTGT	GCCTAGAGAG1860	
TGGAGATTTT	TGATGAAAGG	TGIGCTCGCT	CTCTCGTTTC	TATCTTCTCT	CTCCTCCTTG1920	
TTCTGCACAA	CCACAAGATA	AAGGTAGTGG	TGTGTCTCGA	CCCCATCAGC	CTCTACCCCA1980	

CTCCACAGCA	CACACAAGTC	CTCAAAAGTT	TCAGCTCCGT	GTGTGAGATG	TGCAGGTTTT2040
TTCTAGGGGG	TAGGGGGAGA	CTAAATTCGA	ATATAACTTA	AAATGAAAGT	ATACTTTTTT2100
TAAATTTTCT	TTTTAAACT	TGGTGAAAT	ATTTTCAGATA	CATATTTTGA	TGTCAGGCA2160
GATTAGTTAT	TTAGCCACCA	AAAAAAAGTA	TTGTGTACAA	TTTGGGGCGT	CAAAATTTGAC2220
TCTGCCTCAA	AAAAAAGAAA	TATATCCTAT	GCAGAGTTAC	AGTCACAAAG	TTGTGTATTT2280
TATGTTACAA	TAAAGCCTTC	CTCTGAAGGG	AAAAAATAAA	AAAAAATAAA	2328

(2) INFORMATION ON SEQ ID NO. 237:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 1767 base pairs
 (B) TYPE: Nucleic acid
 (C) STRAND: individual
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 (A) ORGANISM: HUMAN
 (C) ORGAN:
- (vii) OTHER ORIGIN:
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 237:

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TGTGACATTG TCCTGAGGTT CATCCGCCTA AATTATTATT AGCCATCCCT TACCAAATAT 60
TTCAAACCCAG GCAAATGACT TCTGGAAGAG AGAGAAAGGA AGGGGAGAGG GAGGGAGAAAT 120
ATGAGTAAGC AAGCAGGGTC ATATGGTTAA ACATGGAATT TTTTAAAGGA GTTATTACAA 180
GTGGGAGTCA AATAGAAGCT TGGTAGAATG CTTTGGGTAC AGGAATATGT TATGCAATAA 240
AGTGAGGAAG AGAAAAAGGG AATAAGAAGG GAGGAATGTA ACTAGAGCAG CTCCCAACAG 300
TTTGCCATTG TATTTGCCAG CACCAAAATT CGTAGAGTAA GCCACTTACA TTTCCACTGC 360
TAGATTAAAG GAAAGACAGC ATGGGTGATT CTTATAAAGT GAGTATACAT TTATTCTTAT 420
TCTGATATGT GAATTTTTCT TTCACCAGTT AATTAAGTGG TAATTTGTAA ACAGTGGGAA 480
GAAGATTAGA ACAATTATGG AGGTACTGAA TTACACAAGG AGATTAAAT GAAATGAATC 540
AAACTAACCA CAAGATAGGT AGATTGATTC ATTTCAATTT AATCTCCTTG TGAATTCAG 600
TACCTCCATA ATGTTCTTAA TCTTCTTCCC ACTGTTTACA AATTACCAGT TAATTAACCT 660
GTGAAAGAAA AATTACATAA TCAGAATAAA AATAAATGTA TACTCACTTT ATAAAAATCA 720
CCACTGCTGT CTTTCTTAA TACTAGCAGT GGAATGTAA GTGGCTTACT CTACAAATTT 780
TGGTGCTGGC AAATACAGTG GCAAACTGTT GGGAGCTGCT CTAGTTACAT TCCTCCCTTC 840
TTATTCCCTT TTCTCTTCCC TCACTTTTATT GCATAACATA TTCTGTGACC CAAAGCATTC 900
TACCACAGTT CTATTTGACT CCCACTTGTA ATAACTCCTT TAAAAAATTC CATGTTTAA 960
CATATGACCC TGCTTGCTTA CTCATATTCT CCTCCCTCT CCTCTCTCTT 1020
CCAGAAGTCA TTTGCTCTGT TTGAAATATT TTGTAGGGAT TGCTTATTAT ATTTATTTAG 1080
CTGATGAACC TCAGGACAAC GTCTACACAC ACACACATAC ATACACGCAC ACAAATCTC 1140
AGCTGTTGAA GAGTGGGCTT GGAATCAGAC TTCTGTGTCC AGTAAAAAC TCCTGCACTG 1200
AAGTCATTGT GACTTGAGTA GTTACAGACT GATTCAGTG AACTTGATCT AATTCTTTTT 1260

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GATCTAATGA ATGTGCTGCTG TTACCTTGTT TCCTTTTAA TGATAAGCTC CAAGTAGTTG 1320
CTAATTTTTT GACAACTTTA AATGAGTTTC ATTCACCTCT TTTACTTAAT GTTTTAAAGTA 1380
TAGTACCAAT AATTTCTTAA ACCTGTCTCT AAGTGGTTTA GCTACCATTC TGCCATTTTT 1440
AATTTTTATT TAATTTTATT TGTCTGAGCA CACTGATCAA GCCTTGCTTCC 1500
ATTGTCCTGC AATGATATAA GGGTTACATT TTGTGTATA TGGCTTTTCA AGTTGGGATT 1560
TCAGAGCACT GATACAGAGT ATTTTCAGTT TGTTCTCTGG GGGAAATTTCA TTGTCATCTA 1620
TGTTTTTAGC TA'TCTGTGAT AACTTGTTAA ATATTAAAAA GATATTTTGC TTCTATTGGA 1680
ACATTTGTAT ACTCGCAACT ATATTTCTGT AAACAGCTGC AGTCAAAAAA AAAACACTGA 1740
AAGTTTTCAT TTTGCACTGG AAAAAAA

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1767

(2) INFORMATION ON SEQ ID NO. 238:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 2311 base pairs
 (B) TYPE: Nucleic acid
 (C) STRAND: individual
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 (A) ORGANISM: HUMAN
 (C) ORGAN:
- (vii) OTHER ORIGIN:
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 238:

CATCGCCTTC ACCGCGCGCG GCAACATCGT GGTGGCCACG GCGGACGGCA GCAGCGCGTC 60
 GCCCGTGCAG TTCTACAAGG TGTGCGTGAC GTGAGTGAGC GAGAAGTGCC GTATCGACAC 120
 GGAGATCTCTG CCTCCCTGT TCATGCGCTG CACCACCGAC CTCACCCGCA AGGACAAGTT 180
 CCCC GCCATC ACCACCTCA AGTTCCTGGC CCGGCACATG TCGGAGCAGG TGCTTTTGTG 240
 CGCGTCCAGC CAGACCAGCA GCATCGTGGA GTGCTGGTCC CTGCGCAAGG AGGGACTCCC 300
 CGTGAACAAC ATCTTCCAGC AGATCTCCCC CGTGGTTGGC GACAAACAGC CCACAATTCT 360
 CAAATGGCGG ATCTATCGG CCACCAACGA TCTGGACCGT GTGTCGCGCC TGGCGCTGCC 420
 CAAGCTGCCC ATCTCGCTCA CCAACACCGA CCTCAAGGTG GCCAGCGACA CACAGTTCTA 480
 CCTTGGCCTC GGGCTGGGCC TGGCCTTCCA CGACGGCAGC GTCCACATCG TGCACCGGCT 540
 CTCACCTGCA ACCATGGCCG TCTTCTACAG CTCGCGGCCC CCGAGGCCTG TGGATGAGCC 600
 GGCCATGAAG CGCCCCCGCA CGCGGGGCCC CGCCGCTCCAC TTAAAGGCTA TGCAGTATC 660
 GTGGACGTCA CTGGCCCTTG TGGGGATTGA CAGCCACGGG AAGCTGAGCG TGCTCCGCTT 720
 CTCACCTTCC ATGGGCAACC GGTGGAGGT GGGGCTGGCG CTGCGGCACC TGCTCTTCCT 780
 GCTGGAGTAC TGCATGGTGA CCGGCTACGA CTGGTGGGAC ATCCTGCTGC ACGTGCAGCC 840
 CAGTATGGTA CAGAGCCTGG TGGAGAAGCT GCACGAGGAG TACACGCGCC AGACCGCTGC 900
 CCTGCAGCAG GTCTCTCTCA CCGGATCCTT GGCCATGAAG GCCTCGCTCT GCAAGCTGTC 960
 GCCCTGCACG GTGACCCGCG TGTGCGACTA CCACACCAAG CTCTTCTCTA TCGCCATCAG 1020
 CTCCACCTTG AAGTCGCTGC TGCGCCCCCA CTTTCTCAAC ACGCCTGACA AGAGCCCCG 1080

CGACCGGCTG ACCGAGATCT GCACCAAGAT CACCGACGTC GACATTGACA AGGTATGAT 1140
 CAACCTCAAG ACGGAGGAAT TTGTGCTGGA CATGAACACA CTGCAGGCGC TGCAGCAGCT 1200
 CTTGCACTGG GTGGGGCACT TCGTGCTGTA CCTGCTGGCC AGCCTACCCA ACCAGGGTTC 1260
 CCTGCTGAGG CCGGGGCCACA GCTTCTGCGG GACCGGCACC TCGCTGGGCA TGCTTCGGGA 1320
 ATTGATGGTG GTCATCCGCA TCTGGGGCCT TCTGAAGCCC AGCTGCTGCG CGGTGTATAC 1380
 GGCCACCTCG GATACCCAGG ACAGCATGTC CCTGCTCTTC CGCCTGTCTA CCAAGCTCTG 1440
 GATCTGCTGT CCGGATGAGG GCCCAGCGAG CGAGCCGGAC GAGGCGCTGG TGGATGAATG 1500
 CTGCTCTGCT CGCAGCAGG TGCTTATCCC CAGCCTGGAC TGGCTGCCAG CCAGCGACGG 1560
 CCTGGTTAGC CGCCTGCAGC CCAAGCAGCC CTTTCTGCTG CAGTTTGGCC GGGCGCCCA 1620
 CTGCTGCTGC AGTGCTGCCA CCTGCAAGCT GCACGGCCCTC GCCAGGGCCC CAGGCCAGGC 1680
 CAAGATCGAC CACCTGCGGA GGCTGCACCT TGGCGCTTGC CCCACGGAGG AATGCAAGGC 1740
 CTGCACCAAG TGGGGCTGTG TCACCATGCT CAACTGCCCC AACAGAACCA CGCGGTGAA 1800


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GCAGTGGGAG CAGCGCTGGA TCAAGAACTG CCTGTGCGGT GGGCTCTGGT GGCGGGTGCC1860
CCTCAGCTAC CCTGAGCCC AGCTGCCCT CAGTACTCC TCAGTACCC CTCAGTGCC1920
CCTGAGCCCG GCTGCTGCAA GAGCCACCGC TCGCCCTGGA CTCTCCTCGG CGCGGTTAAC1980
CTCAGCCCGC CCTGCAGGGC TGTTGAAGGC CGTGGGCCGG ACGCCTGCGT GACCAGCAGA2040
GCTTCTGAGG AAGCCCCCTGC CTTTGTCCAG CTGGGCCCGC AGTCCACACA CCACTCTCCC2100
AGGACCCCCA GATCCCTGGA CCATCTGCAT CCAGAGGACC GTCCGTGACG GCCGGGGGTC2160
CAGGCGGACC TTGTGGTGAC CCGGCTCGGG CGTCTCTCG GTTTCCTTGC CTCACCCGCG2220
GAGAGCGCTG AACCTGGACA AGCAGCGGCT GGAAGGACA GGTCCAATAA ACGCCCTCTG2280
CGCCCAAGAA AAAAAAAAAA AAAAAAGGG G

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2311

(2) INFORMATION ON SEQ ID NO. 239:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1772 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 239:

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TGGGCGCTGT AGTCCGCGCG GAACCTGTTT GCGACCCCGA GTCCCATGAC ACCGCTTCTC 60
CTCACACCCC AGTCCGCGAGT GCCCCTCCCC AGCCTCGGCC GGGCTCCCCG GGAGCCGGGG 120
GTGGCGGTTC AGCTAGTGAG CCGTTTCTCC CTTGGGCTCG GAGGCGGAAG CTGTAGGGGG 180
GCGGGGAGGA GCTTCGCGTG CCGGGTGAAC GCCCGCTCTA CGTGCTCGTT CTCTTCGCGA 240
CCGCTGCGCG CGAGCCCCGT GTCCCCACGG CCGGCAGCAG CGCCGGCGGC TGGCGGTGAA 300
CGCGGAGGGG GCGGAGGGAG CCCGCGCGCG CGGCAGCAGC TACAGCGAAA GCGCGGAGAG 360

CGTGGGTGAC ACCCGGCGGC TGATCACCAA GCCGAGAAC CTGAATGACG CCTACGGACC 420
CCCCAGCAAC TTCTCGAGA TCGATGTGAG CAACCCGCAA ACGGTGGGGG TCGGCCGGGG 480
CCGCTTCACC ACTTACGAAA TCAGGGTCAA GACAAATCTT CCTATTTTCA AGCTGAAAGA 540
ATCTACTGTT AGAAGAAGAT ACAGTGACTT TGAATGGCTG CGAAGTGAAT TAGAAAGAGA 600
GAGCAAGGTC GTAGTTCCCC CGCTCCCTGG GAAAGCGTTT TTGCGTCAGT TCCTTTTAGA 660
GGAGATGATG GAATATTTGA TGACAATTTT ATTGAGGAAA GAAAACAAGG GCTGGAGCAG 720
TTTATAAACA AGGTCGCTGG TCATCCTCTG GCACAGAAGC AACGTTGTCT TCACATGTTT 780
TTACAAGATG AAATAATAGA TAAAAGCTAT ACTCCATCTA AAATAAGACA TGCCTGAAAT 840
TTGGCAAGAA GGGGCAAAAA CGTGACTATT AATGATTGAT AAGCACCAGT GAAGAAGTTC 900
TAACCTTTAG CATGCTGCAC AGAAACTGGT ATAACATGCC TTCAGTATAC TAACACTCAT 960
ATGCTCAGTT TTGTTTGTG TTGGCAGTTG ACAAGAAGTT AATTTGCTTT AGTAAAAATC1020
CCTCATTCCA GCCTTTCTAT ATAAATAGCT CTTTCTTGCT GTTTTAAATGT GGTGCACACT1080
ATAGCCCTAC AAACCTGTGA TTCCAGTGTA ATCTGCAGTG TCGTAACTAA AGTTACTGGC1140
TTGGTCTTAT TTGCACAGTT TTTGCGTCTT GTTTGCTTCT TGCATCTGAT TAACTAGAA1200
ATTTCCTCTT CCCCCTTTTA ATTTGTGATG TCACCTTGACC CCATTTATGT GTAGGAGCAC1260
TACACCAATT GTTTCCAATA CTGCACACAT AAGATACATA CTGTGTGCA GAAAGTATCT1320
TCCTCCAGGC TTGTAATACC CTTACATGG AAGATTAATG AGGGAAATCT TTATATTCTG1380
TATAAAAAACA AAAGCAAATT TATATACTAA AATCATTGT CTAATAATTT AAGTTGTTT1440
CAAATAAAAAA TTAATAATGA TTTCTGATAT GCACGTGATT TGTGCTCTCC AGCTTTTTTT1500
GCTCTCTATG AGTGACTACT TAAGTCACTT GTTGAGAGGG ATTATTACT AATTATATAC1560
TTCTCATTCG TGTAATCCA TTCCCTTTAA ACAGTGGTGA TATCAAATAT ACTTCCATCC1620
ATTGAATGGG GTATTTTTTA CAACAACAAA AGTGATATAC TAAAAAATGT ATTGCTTAAG1680
GCTTATTGAA TCATTTTGAA GCACTTTGTG TATTTGAAAA CTGCTTTATA ATCTCATTTA1740
TTAAAGGAC TTTCAAAGT AAAACCAAAA AA

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(2) INFORMATION ON SEQ ID NO. 240:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2409 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 240:

TCTGTATCTT	CCTTGCCCTC	AAATACCCCTG	AGGTGATAAA	CTGTTCCAGT	TGTAGCCAAC	60
TACCACTGGG	CCCGGCCTTA	ATAAAAAAT	TGTAGTCATT	AATGGTGTGT	TTGAATTGAA	120
GAGATACCAG	GAGATAGAGG	TGAAGTGCAG	TACTTTTATT	CTTTAAGAA	ATAGTCTTTA	180
GCCAGGTGCA	GTGGTGTGTG	CCTGTAGTCT	CAGCTATTTC	AGAGGCTGAG	GTGAGAGGAT	240
CACCTGAGTT	CAGGAGTTCA	AGACCAGCCT	GGGCAACATA	GCAAGTCCCT	GGCTCAAAAA	300
AAAAAAAGTT	TCCCATTTCAT	ATTAACCTCA	TCTTTTAAAA	ATGTCATGAT	TACAAAGTGA	360
AAAGATTGTT	CTTTCTTAGA	GGCTCAATCA	CAGAGGTGAA	AGTGACCTTG	GAAATCATAT	420
ACTCTATCCC	CATGTTACAC	AGATTAGAAA	AACTGAGGTT	ATGGCACTGA	CTTAGGCACC	480
CCCCAGCAAG	GCAACCCAGG	GACTACAAC	GGCAATCCCA	ACTCTCGGGC	TAGGGCTTTG	540
TCTACCTTTT	TTTGCATTGG	CTCTTAAAG	AGGCAATGAA	TACTAATTC	TGGCATCAGA	600
AAAAAAAGAA	GGCATGAGGT	GGGAGGATTC	TTTTTCCCT	GATGGGAAAC	AGTGAATAAG	660
AAAAATCTCA	TCATTGCGATG	GAAGAGGTGA	CTTAATAATT	TTAATTATGA	ATTTGATGTC	720
CCATGTTTGT	TAGTTTTGTT	ATCATTTGAAC	CATTGGGGCT	GGAACTCTGC	TAAATAATTT	780
TATCTTGGTA	GCCAGCAATT	ATGTTGGTAT	TTTATGTGGG	CCCTCCCGAG	TTTTCATATT	840
AATGAAATGA	CTAATAGTCG	TACTTAAAG	GTAACCTAC	TAAAGCAGAA	TGAGATCTAA	900
TATGTTGTGG	AAATAAAAGA	GTTTGCAGTG	GAATGATACT	CTCACTCCGT	GCTTGTAAAA	960
TTGAGTTCTA	TTCAAGACGG	AACCTGCTATG	ACTGGCCCTAT	TCAAGGCTTC	ATATTTTTTAT	1020
ACAGACTATT	TCACAGACCA	TAGATTATTT	TTAAAAAGGA	AAATCTCACA	CATAAATAAG	1080
CAGTGGAAAA	TGTGCTCAAT	GCTATGGTGC	GTCAGGCCCT	CTGCTCTACCA	GGTTTCTCCC	1140
GCTTTCTGCA	GAGCTGTGGA	CCCTGTACGT	ACCAACACAG	TGAACCTGGT	CCATCTTTCT	1200
TTCTTCTCTT	TTTTGCACAT	TTGCATTTAT	ATCTCTCTGT	ACTAAAGAA	ACAAATTATT	1260
TATAATTGGG	GTGACAAAT	AAAGGAACAA	AGATGGGGC	AATAGTTGCT	TCCTAGCTGG	1320
AGCTSTAAGT	CCATGTTACA	GAACCTCACT	ATTTAAAAAG	TTTTAAAAAG	TTTATGAACC	1380
TTGTCTCTCA	ATTCGCTGAA	TACTTATTTG	TCTTTTAAAC	TCCCTCGGT	GTATGGATCA	1440
TCTTGGTCAG	AATGCCGTTG	TTTCATTGTG	AATCAGGGGA	AAATGTAAAT	CATTGGAGAG	1500
CTGTTTTCTT	ATTACCAAA	GTACAAATCA	TAAGACAAC	GAAAGCAACA	ACTGCTGGGT	1560
TCAGTGACAA	AGATTATAAA	AATCATCAG	TTCAAAGTAG	AGTTTTTAGC	CAAGGTCAAG	1620
AACTAACCTG	GGGCTGAGTC	AGCGTCTCTA	CCCACCTAAA	TAACAGCGTA	AAGATCTTTT	1680
ACTAAATTCT	TTATGTGGTC	TGCTGTGGATG	TAAACCTATA	TATTTCCCTT	TGAACAGAA	1740
TCATATCTCT	CAGACTCTTG	GCACCTCTGC	ATAGCTTTGA	CCGAATGTTT	ACTCTCATCG	1800
TAATGGGAAG	TTTCTATCTA	TGCAGATAAT	ACATGTTTTT	AAATACTGTT	TTCTGTTTAG	1860
TCCTCAATCT	TCCTAACTCA	AATTGGGGAC	TGAGGAGAGA	GAAAGGTGGT	TACCCCTGTT	1920
ACCGTGCCAT	ATTCTTCTTG	CTGCTTTTCA	ACCCACAGTC	ATTGTTGATT	GACGGTCTCT	1980
CTATAATGTG	CGTGCCCTTC	AAGTTCAGA	AAACTTTCCC	AATCATTTCA	CTTCAATCTT	2040
AATTGAACCC	AAGAGTCAAA	GTTATTATTT	TCTCCGACCG	TGTTTGTGAT	CTTCTGTTAT	2100
ATTTTGGGGC	ATGTTACTTT	TATGTTATAT	AAGCTGTAGT	GCATACCTTT	TGTATTGCAA	2160
AAAACCTGCT	AGTAATTTAT	GTACATGTAT	TCCACATTTT	AGTGTCCTTG	AAGTGACAAT	2220
CCATAGTTTG	TGTAGTTTGT	TTATTTGTCA	ACTTTACCCT	GTGTTTTAAG	GACATCTAAA	2280
CATTCTCTTG	TCCTATCAAG	TGACAAAAGC	AGAATGTAAT	TTTTTTTGG	AAGCTTCGTG	2340
ATTACCTGTA	ACAAGTTCTG	TTTTTAAAC	GAATACAAAT	AAAGTTAGTA	ACTATTTTAA	2400
AATCAAAAA						2409

(2) INFORMATION ON SEQ ID NO. 241:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 2594 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 241:

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CGCCCTTTTT TTCTTTATTT TCTTATGTAC TCATCTACTT ATTCTCAAAG TATTTAGCAT 60
TCAACACTCT TTTTGGCTTA AAAAGAATGG CCTTACAAAG GGACAGAAAA GAGAGACAC 120
GAGCTTGGTG TATTTTTCATC AAGTTATGTG GCAGAGAAAT CCAGATATTA CCAGGACCTG 180
TCTAAACAAA TGTGTGGGGT TTTCTTTTCA TTCGGATAGC CACTTTATAG TTGGAATATC 240
AATTCTAATG AGGAGGAAGA CATAAATATA AGTGGTAAAA AGAACAATGA CTCCCTTTAA 300
AACAGGCTGG ATAATCTATA TCAGCCTTGT GGGTGGAGAC TAGTATTTGA TCCTTGGCAT 360
ATAAAACATT TTAATATGGT TTACATGGGA AAATATCGAT GGCTTCCTCA CAAAATGTAT 420
GGGTGACGTG AAGTTGAAGA GCCAATGGCT TGGGTGACAC GTGCTGGATC CAAAAGATC 480
AGGGAGACTA GAATAAAACT TGGATGTTAA AAATTCCACA GGAATCCACA TAAAGTACTA 540
TATTTGGGCT AAAATGAAAA ACTAAATACA AGGTGGGAGA GAGGCAAGAA TTTCAATTGA 600
CTAAGCTCAG TGTGAGTTCA AACTGGGATG GAACCATGCA AAAACAAAC CCACAGACAT 660
CGAGGCTACG TGAGGAGAAA ACAGTGGTGA GGATCACATC ACATTGTGTT TGCATTGTGC 720
GGAAACCATAC TTAAGAAGA AAACCGATCA TCTATAATAA CATCAGTTTA TCAATGCCCC 780
GTCTGATGA AGTGTGCAGA CTCTCAGAAA CAGCAGGAAG GACTTCATGA GAACCCCTCAG 840
GCTGGAGAAG GGAAGTGGGC ACAAGGAGAG CTCTCCTAGG ACCAGGACCA AGAAGCTACA 900
GGCAGGCACA GTTTAGCTCC TGCAGAGACC CAGCTTTTCA CAAGTTGGAG CCTTCCAGAG 960
ATAGAGGGAC TGTGGTAGGT GGTGACCCAC CCATCACTGG AGGTGGAAGC AGAGGCCGTT1020
TGCCAGGGAT GCTGGAGAGG GGATTCAAGC ATCTGGCTGG GCAACGTGAT GCTCAGGCC1080
GTCTCCACTC AGGGCTTAGG GGAGTCTGTG AGTAGAAGAG CTTTAGGTGA TTTGTTTGGT1140
GGGGGAAGGC AAGTACACAG CTATGCACCT TCCGTTTCTG ACTTTTGGCA CCTGTGACG1200
CATGGGGAGC CCACGTGTGG ACTGAAACCC TGAGCTGAAT GCGGCCCTAT GTCTCAGAGA1260
AACACTGGCA AGTTGGTCAG AGCCGCCGTC TGACATCGAGG CGTACTGAGC GGCAGGATGG1320
GGGGCTGCC T GCCCAGGGTC TCTCACCGTG GTGTAGCAG AGCCATGGCT TGCTTAGGAC1380
CCTATAGATA CCATCACTCT TTCTCAGCTC GACTGGAGTT TCTGCACCTT TGCAGGGGCA1440
AAGTAACCTC CTGCACCCCTG AACCACCCCC CATTCCTGTT CATTTACAGA GATAATGAT1500
GAGGGGGGGG GGTGTCCATC GTGCTGAGG TGAGCCGCA AGAGGGTGA AACTTCCAGC1560
CAACTTTCTC AGTCTTTTCT CTTCGAGAG GGAAGGCCACC TGCTATACAA ACTAATACCC1620
CCTGCCCTGA CCCCTTCCCC ACGACTCAGT TGACAGAAGG ATATACTTTG TTATAACTTA1680
TTATTTTGTT CTCTGTAAT ACAAGATGTT TATAGGAAT ATGTATTCTG AACTCTATCT1740
GCAGAAATGAG TCACTACACC AAAATAGTTC TATTATTTAG AATGTGTAA TTTTAAAGGG1800
ACCTGATAGG TATTTATTTA CATATGCGAT CCACATTGT GTGAAAGCAT GTGATCATAC1860
TAACCCAGCC TCGTGAATG TCGCTGTACG ATGATTGATG TCTTTTCTCT AGTCCATAGT1920
TACAAATTGT TAGTATGCTA ATCAGTCCAG TTCCCTGAGG TTAAAGATCA AATATAAATT1980
ACTCTGCTTT TCGACTCATT CAGGTAGCAT TGTACCTGAA CCTGATTGCT ACTTTTTTCA2040
CTTAAATATT ATATTTCTCT ATCTAATCTG CCTTCCCTCT ATCCACAGAC ATTTGGAGAA2100
GGAAATGGGA GGGTGTCTGT TATCCCTTTC TCTTTGCTTT GTCCCGCTTG TTAGACTGGC2160
AGCGTCAGTT GCTCGGTGGG CTGTTGTTAGA GCGCTGGGGT AGGCAGGTGG CTGGCGGGGA2220
CAGGGAGAGG CTGAGAGGGA AGTGGTGCA TTTACTGCTC TGACACTTCC ACTGTCCTG2280
CTGGGGATGC TGGGGCCCAAG GCCTGTGGGG CCTGTGAAGT GCACAGCCAG GAGCAGGAA2340
CCCATAAAT ACTCCGTAC CTCCATGTCC CCTCTAAGCT GTTAAATTAT TACATAAGCA2400
GGTGAAAGGT AGAAGGCGAA TTATGTGAGT AAATATGGTC TGTTTTCTCT TCAAGAGAA2460
TGACTATTTT TGTGTGIGAC TAATTTATTT TTATTATTGT AAAGATACAA TAACCCGGTT2520
GAAATATCTG CTTTGTTGAC AAGCGTGGC TTTCTATGGC NTTATTNGCG TTTGTTNTC2580
CTGNAAATAG CGCC

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2594

(2) INFORMATION ON SEQ ID NO. 242:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 1012 base pairs
 (B) TYPE: Nucleic acid
 (C) STRAND: individual
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 (A) ORGANISM: HUMAN
 (C) ORGAN:
- (vii) OTHER ORIGIN:
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 242:

TGAACTGGAG	AGGTGAAGGT	TGCAGTGGCC	TGAGATCGCG	AAACAGAGCG	AGACTCCATC	60
JCAAAAAATA	AATRAATAAT	AAAATTTGCC	GTTTACGGTG	GCTTATGCCT	GTAATCCCAG	120
CACCTTTGGGT	GGCCGAGGCG	GGTGGATCAC	CTGAGGTCAG	GAATTTCGAGA	CCAGCCTGAC	180
CAACATGGAG	AAAACCCCGT	CTCTACTCAA	AATACAAAAAT	TAACCCGGGCG	TGGTGGCGCA	240
TGCGTGTAGT	CCCAGCTACT	TGGGAGGCTG	AGGCAGGAGA	ATCACTTGAA	CTCAGGAGGC	300
AGAGGTTGCA	GTGAGCTGAG	ATCATGCCAT	TGCACTCCAG	CCTGGGCAAC	AAGAGTGAAA	360
TTCGGTCTCA	AAAAAAGATG	TTTTTCATTT	TTTTTCATTT	ATCTATCCAA	420	
GCACTGTTCC	ATGGTCAGCA	AGTCATATTT	CATAATGTGG	ATTTTCCAAA	ATAATTATTG	480
AATACAGCTA	TTCTATGGCT	ACTTTTAGTG	TTTTTTGTGGT	ATGTGGTGTG	GGAGTGTTTA	540
TGGAATTACC	AGTATCTTAA	ATTTTCAAAG	GAACCTTGGA	AGTCTATCAC	TCTAAATGAA	600
AGTCTGTAC	TCTACATGAA	TTATGTGCTC	AAATTTGACC	AACTCAGTTT	AAGACACAAA	660
ACAGTAATTT	GAAGAAGGAA	AAATGAAGAG	AGTTTCTAGT	TTAATGGGTT	AAATTTTGT	720
TGTTGCAATA	GTAAGTTTAG	TCTTCTTATA	ATATTCTTAA	ATGAAAAATC	ATAGGTATTT	780
GTTACCATGT	GTGAAGATTA	CTTTGTTAAA	AGCAAAAGTG	GTCGTGTGAT	ATGCTAAATG	840
TTAATTACTG	ATTTTATATG	TTTAAATCAC	GCCAAACAAA	TTATGTCTGT	GCCATCCAGG	900
GTCTGTGTGT	AATCTTTTTC	TGAGTACTTG	GATTGGGATA	AAGGGCTTGT	ACTATGCACT	960
TTTTTATTAAT	GAATAAATAG	AAAACGTTAG	TAACAAAAAA	AAAAAATAAA	AA	1012

(2) INFORMATION ON SEQ ID NO. 243:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 1206 base pairs
 (B) TYPE: Nucleic acid
 (C) STRAND: individual
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 (A) ORGANISM: HUMAN
 (C) ORGAN:
- (vii) OTHER ORIGIN:
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 243:

TGAGACGGAG	TCTCGCATCT	GTCGCCCAGG	CTGGAGTGCA	GTGGCGGGAT	CTCGGCTCAC	60
TGCAAGCTCC	GCCTCCCGGG	TTCACGCCAT	TCTCCTGCCT	CAGCCTCCCCA	AGTAGCTGGG	120
ACCACAAGCA	CCCGCCACTA	CGCCCGGCTA	ATTTTTTGTA	TTTCTAGTAG	AGACGGGGTT	180
TCACCGTTTT	AGCCGGGATG	GTCCTCGATCT	CCTGACCTCG	TGATCCGCCC	GCCTCGGCCT	240
CCCAAAGTGC	TGGGATTACA	GGCGTGAGAC	CGCGCCCCAC	ACTATGAGTG	TTTTTAACAC	300
CATTCTCCCC	CACCTTCTCT	CTGGGTGACA	TAAGAGAGAA	ATAACCNCTGT	AGTACAGCAG	360
CTAAAGTATT	CTCCTTTCAG	AGAANNTTTT	TTTGAGGTC	TCTAATATAT	ATTTCCCCCN	420
TTGTCTCTGT	GATCTCTTAT	TTATACTATA	TTATTGTCCC	ATGTACTTTC	TAAACTGAGC	480
TTGGAACATT	TAGTATTCCCT	GCAATTGGAC	TTCCCACTTA	ACAATTATAC	AGACTTTGCT	540
TTTAGAATA	GATTAGGTTT	CAAAACAGAA	GTTCNAANGT	GTAACAACNA	ACAATAAAAA	600
TAGATTATGA	AACANGGCTA	TAATTGGCTC	TTTTGGATT	NGATAGGGGC	AAGATGAAAG	660
GNCAACNTTT	CTTGCNTTTT	GAAANNTCAT	NGTTNGGGTA	ANGAGGTAAG	GNAATNCCAG	720
CTANCAATTT	TNATTAGTGC	TTGNAAANCG	GGCTTNCCTT	NGAATTCNCT	CANGGNCCTT	780
ATCATTTTTT	TTTTCTTNAC	TAAATNCAGAA	GAGAGNCTGG	GGTAGAAGNC	CCCATNGTTT	840
GTATTCNAT	GAACACACNGT	CGGGTTGGNA	GTAAAGGCAG	AAACAGCNTA	GACACACCAG	900
GNTGTGCTG	NNTTTGACAT	TTATAAGCTG	GCACTCATCA	ACACTCCTGT	TTCTCCTTTC	960
TCTGGGACGT	GTGGATTAAAG	GGGTGTGAGT	TGTGGGAAGA	ATTGNCCTTC	GTACCTCCTG	1020
GATTATTAT	TTTTCTCAAA	TACCAACCN	GTAAGATCCC	AAATAACTTG	AGAAAAATTG	1080
TTTCCTGATC	TGTCCACTTC	TGGTGTCAAA	GATTTTACTC	ATCTTCTTAG	TACATTCTAT	1140
GTATTTTATA	TGTATAATTT	TNATACAATT	AAAAATAGAT	TTTTGTNCTA	GTNGAAAAAA	1200
AAAAACA						1206

(2) INFORMATION ON SEQ ID NO. 244:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 2514 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: partial cDNAs produced from individual
ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 244:

AAGGTGAAGA	GCGGCATCCG	GCAGATCCGG	CTCTTCAGTC	AGGATGAGTG	CTCCAAGATC	60
GAGGCCCGCA	TGATGATGAGT	GGTGTCCCGG	GCCGAGAAGG	GCCTGTACAA	CGAGCACACG	120
GTGGACCGGG	CCCCCTGCG	CAACAAGTAC	TTCTTCGGCG	AGGGCTACAC	GTACGGGGCC	180
CAGCTGCAGA	AGCGCGGGCC	GGGCCAGGAG	CGCCTCTTAC	CGCCGCGGGG	ACGTCGACGA	240
GATCCCGGAC	TGGGTGCATC	AGCTGGTGAT	CCAGAAGCTG	GTGGAGGACC	GCSTCATCCC	300
CGAGGGCTTC	GTCAACACGG	CGGTATACAA	CGACTACCCG	CCCGGCTCT	GCATCGTGTC	360
CCACGTGGAC	CCCATCCACA	TCTTCGAGCG	CCCATCGTG	10231512CT	TCTTTAGCGA	420
CTCTGCGCTG	TGCTTCGGCT	GCAAGTTCCA	GTTCAAGCCT	ATTCGGG161	CGGAACCACT	480
GCTTTCCCTG	CCGGTGCACA	GGGGAAGCGT	GACTGTGCTC	AGTGGATATG	CTGCTGATGA	540
AATCACTCAC	TGCATACGGC	CTCAGGACAT	CAAGGAGCGC	CGAGCAGTCA	TCATCTCTAG	600
GAAGACAAGA	TTAGATGCAC	CCCGGTTGGA	AACAAAGTCC	CTGAGCAGCT	CCGTGTTACC	660
ACCCAGCTAT	GCTTCAGATC	GCCTGTCCAG	AAACAACAGG	GACCTGTCTC	TGAACCCCAA	720
GCGGTCCCAC	CGCAAGGCAG	ACCTGTATGC	TGCCACAGG	CCACGGATCC	TGGAGATGGA	780
CAAGGAAGAG	AACCGGCGCT	CGGTGCTGCT	GCCCCACAC	CGCGGAGGGG	GTAGCTTCAG	840
CTCTGAGAAC	TACTGGCGCA	AGTCATACGA	GTCTCTAGAG	GACTGCTCTG	AGGCAGCAGG	900
CAGCCCTGCC	CGAAAGGTGA	AGATGCGGCG	GCAGTGAATC	TACCCGCGCG	CCTCCTGGGA	960
ACTCTGGCTC	ATCCTTACGT	AGTTGCCCTC	CCTTTTGTTC	TGAGGGTTTT	GTTTGTGTTT	1020
ATTGGGGGCT	TTTTGTTTTT	TGTTTTTTGT	TTTTTTTGAT	TCATATATAT	TTTCCTTGGT	1080
TTTGTGCTCT	GTTAAGCCTG	AAGAATAGAA	TTGGCCAGGA	CTAGGTCTCT	CATATTTCTG	1140
GATATCTCTC	TGGATGGAAG	GGCTGTTGGC	ATCAATAGGG	GACAGAGGCT	GATGCTGGAGT	1200
TGGCCAGTAG	AGGTGGTGGA	GCAGAGCAGC	CATCTTTTAA	GTGGGGCTGT	ATCAGGCTGG	1260
GTTTATTTAA	AAGCAACAAA	ATGTTTTGGT	TAAGAAAAAT	ATTTTGTCTT	CAGTGTAATAT	1320
CTTCGCACTG	TTCTAAACAA	AGTTTCAGTCT	TCTGCTCGCC	CCTTTTCCCTC	ACTGATGTCT	1380
GCACCTTGTT	GAGGTCTCCT	GGAGCCTCAC	AGGCTCTGCT	GTCTCTCCACT	TCTCACCTGC	1440
CATCCACGCC	CTGCAAGCTC	ATGCAAAAC	CCTTTCTTCC	TCTCTGCGGCA	GAGTGTGTTCA	1500
GGTTGCCTGG	GCAGGGGCTT	AAACAGTGCC	AGCCCTGCCC	ATCCCAAAGC	TATTGTTAAGT	1560
CCCCCCAGGC	GTCTCTCCACC	CACGCCCACT	AGCCTGCCAT	GTCCACAGTT	CCTTGGGCTG	1620
CTGAGGGGCT	AGTGCACTGG	TCCTGACCTC	TCTTATCAAG	AGCACACTTC	TTTGCTGGTT	1680
GCTCCTTTTG	AGCATATGCG	TGTGATTATT	TGGAACAGTT	AGACTTGCCA	CGTTGGGCTCA	1740
GTTTTAGAAA	TTGTTTCTAG	CTAGAGGGAC	TGGTGTCTCT	CCAAGTCTAG	CATTTGGGGT	1800
ATGGAAAAAT	TTTGTTGGTG	TGTTGAGGGT	TTTTGTTTTT	TTTTTTGAGT	TTTTTTTCCC	1860
CCTTTAGTCT	CCTGGCTTTT	TCCTTTCCCT	TCCTTCTCTC	ACTGGCCAGC	TGGGGCTCAT	1920
TCCTCATGTC	ATCCTTCTAG	GAGGCGCCTT	GCCTCATCTT	GCTGTCCGGC	AGCATGATCT	1980
CAAGGCCAGA	GCTCAGGCCT	GCAGACTGGG	CTGGTGCCTC	CTCCGCTTCA	GGGTATGGGA	2040
GTGGTGTAG	GGGCTTTCAA	AAAAATAATA	GAAGAAAAAG	GTAAAGTCTT	TGGTAGCTCT	2100
TATCCACTCA	GATCTTGGAA	GGCAGCAAGG	TTTTTGTGAT	CTAGATTAT	TAGGAATGTC	2160
TTCTTGTGAG	CCAGGCCAGG	ACCCGGGCTT	GCCAAGAGCA	GAGGCCCTCC	CAGCAACCCAG	2220
GATACCACCA	CTTTGGGGGG	TTTGTGTACA	GAGGTCCGGG	TCTGAGACCT	CATAGGCTGC	2280
AGAAATCTGG	GCGAGCCACC	ATCAAGAAGC	CCCTCTCAGG	GGCCAGAACT	CCTTTGCCAG	2340
CGTGGATTTC	TCAAGTCGGG	ACTGCATAAT	TAAAGCAGTT	GCTTTTTTAT	TTTTTTTACA	2400
GCTTTTTTCC	CAAAAATGAT	TTGTAGTTGT	GTGTGCAGCA	CTTCGCCCTG	ATATGTGTGC	2460
TCTACATAAA	AAACCAAATC	TAATATATTT	TGAAAAAAA	AAAAAAA	AAAA	2514

(2) INFORMATION ON SEQ ID NO. 245:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 3903 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 245:

GCAGTTGGAT CCCTGGCCGG TCGGGCCCGG CCCGGCCCGT GAGCGGGCGCA CAGAATTGGGC 60
 CGATGCTGCT TCTACACGGC GGGGACGTTG TCCCTGCCTCC TGCTGGTGAC CAGCGCTCAGC 120
 CTGCTGGTGG CCCGGGCTCT CCAGAAGGCT GTAGACCAGA GTATCGAGAA GAAAATTGTG 180
 TTAAGGAATG GTACTGAGGC ATTTGACTCC TGGGAGAAGC CCCCTCTGCC TGTGTATCT 240
 CAGTTCCTATT TGTTCAAATG CACCAATCCA GAGGAGATCC TCAGAGGGGA GACCCTCCGG 300
 GTGGAAGAAG TGGGGCCATG CACCTACAGG GAACTCAGAA ACAAGCAAAA TTTCAATTT 360
 GGAGATAATG GAGACAAATC ATCTGCTGTT AGCAACAAGG CCTATGTTT TGAACGAGAC 420
 CAATCTGTTG GAGACCCCTPAA AATTGACTTA ATTAGAACAT TAAATATTCC GTTATTGACT 480
 GTCATAGAGT GGTCCCAGGT GCATTCTCTC AGGGAGATCA TCGAGGCCAT GTTGAAGACC 540
 TATCAGCAGA AGCTCTTTGT GACTACACACA GTTGACGAAT TGCTCTGGGG CTACAAAGAT 600
 GAAATCTTGT CCCTTATCCA TGTTTTTCAGG CCCGATATCT CTCCCTATTT TGGCCTATT 660
 TATGAGAAAA ATGGGACTAA TGATGGAGAC TATGTTTTTC TAACCTGGAGA AGACAGTTAC 720
 CTTAATCTTA CAAAATTGT GGAATGGAAT GGGAAAACGT CACTTGACTG GTGGATAACA 780
 GACAAGTGCA ATATGATTTA TGGAACAGAT GGAGATTCTT TTCACCCACT AATAACCCAA 840
 GATGAGGTCC TTTATGCTTT CCCATCTGAC TTTTGCAGT CAGTGTATAT TACTTTCAGT 900
 GACTATGAGA GTGTACAGGG ATGCGCTGCC TTTCCGTATA AAGTTCCTGC AGAAATATTA 960
 GCCAATACGT CAGACAATGC CGGCTTCTGT ATACCTGAGG GAAACTGCCCT GGGCTCAGGA1020
 GTTCTGAATG TCAGCATCTG CAAAGAATGGT GCACCCATCA TTATGTCTTT CCCACATTT1080
 TACCAAGCAG ATGAGAGGTT TGTTTTCTGCC ATAGAAGGCA TGCACCCAAA TCAGGAAGAC1140
 CATGAGACAT TTGTGGGCAT TAATCCTTTG ACTGGAATAA TCCTAAAGAG AGCCAAGAGG1200
 TTCCAATACA ACATTTTATGT CAAAAAATTA GATGACTTTG TTGAACGGGG AGACATTAGA1260
 ACCATGCTTT TCCCAGTGTG GTACCTCAAT GAGAGTGTTT ACATTGATAA AGAGACGGCG1320
 AGTCGACTGA AGTCTATGAT TAACACTACT TTGATCATCA CCAACATACC CTACATCATC1380
 ATGGCGCTGG GTGTGTTCTT TGGTTTGGTT TTTACCTGCG TTGCAATGCA AGGACAGGGA1440
 TCCATGGAAT AGGGAACAGC GGATGAAGA GCACCCCTCA TTCGAACCTA AACATTGCGC1500
 TTGCTTGGTG AAGAACTGTG GTGAGCTGTC CTGACCTGGA CGATGACGTG GGGAAACCC1560
 CCACCTCCTT CGAGGCTTGT TGCCTGTTGA AAGAAGGAAA AAGACAGGAG CCTGGCAAGT1620
 GATAGGAACA TTCTGGCCAG AGGTAAAGA GCAGGCTGAC ATGGCTGCGC ATTAAGCTTT1680
 ATAAATCATG TGGGGCTCTG AAATTTGTTCT TTTATGTGTC TAGCAAGTAT TTAATAAAC1740
 CTTGTATAGT AAAAAAAGAG TTGTTGGGTG CTGGTAGCTC CAGAATTTTG TGAATTTAT1800
 TGTGGGTAAA ATCTCTCTGC ATCACTTGTG AATGCTACTG GTCTAACCTC ATTCAGTATG1860
 CTTCACTTAC CGAATTTTGT GCTCAAAATG CGTATATACC ATTTTATGTT GTATTCTCTG1920

ATTTCACCTG CAAAACAGAA GTAATTAAGA GTTCGGGACC CAGGGTAAAA TGGTAGCTTC1980
 ATCCAATATA TCATTCAAAAT GCATCTGATT TCTAAAAACAT ATTACATTTT ATGCTGATCT2040
 TCAGTTCATA ATTCTTCCAG GAAAACTCAG TCTTCCAATT GCAATAAAAT ACTGGGTAGA2100
 ATCAAAATGGG AAAGGGGTTG GGTGGGGCAA TACCATGAGT TTGATAGTGA TAAGCTCCTA2160
 AGGATTTTGA ACTTGTACTT TTGTGAACGA AGAGAATGCA TAAATAATGT TGGTGAGGAT2220
 AAAGTACAGA TATTTCAATG AGAATTAATT GCTAGTTATG ATGCTTGTGG ATCTTGAAC2280
 GTTTTTTTTT TAGTCAAAAT GATCATGCTA CGAAAGATG CTCTCAGAG AATGTAATGA2340
 GTAACCTGAT TTCTTCTCTG AGTCGCCCTT GCCAAATATG TTACTGTATT AATTAATCA2400
 ATATTGAGTG ATTTATTGTA AAATATGATA TATGCGAAAT CCATCTATCT CACGCTTAAG2460
 TTACACATAA GTTTCAGAAA GTCTGATTAG ACTAAAGAGA TATTTCTCTT GGGACAGCCT2520
 TCTTCTTGTT AATTTTGAAG TCTTTTAC AAGTTCCTTC CTCAGTTTCA GTTCTTTCCA2580
 GTGTTTGTGA GCTCACTGTC ACTCACTGAA TAGAGAAACG TGTGCCCTAT ACTCTCTTG2640
 ACAATCATTT TGCTGAGTCA ATGATGGATG TTTAAATAT TGACACAAAGT ACTTTTGAAG2700
 AAGGCTGTGT AGGACCAGAA GCAGAGACAC CACTTTTCAA AGGACTTCTT GGTTCAGCA2760
 TAACCTAAGA CAGGGAATTT GGAGCCATCA TATGTACAG TGTTCAGAA TCAAGCATAT2820
 TTAAGGGCAT TTCTTTTATG TCTCAAAGTT CAGCATTCAT TTGAAATTGA GACGCCATA2880
 CATTTAGCTG ACAAGATGCT TATAGAATTT CTTAACAACT GAACCATTGA AAAGGATTT2940
 TTTTGTTTAA AACTGGATTT CAATGTAAGC AAATGAAGAA AAAATATAGA TTTCACTTC3000
 ATAGCTTCTT ATCCCTGTAT TAGAGTAATA ATTTGTTTTA GTGACAAATTT TTTCTTTT3060
 TACACTAAAA CAATATGTGA TATATTTCCC CTCTTGAAGA GGCACATTCAT TAACTCTCA3120
 AATTTTCTAT AGAATCAAGA TAGAACCTTT AGATACTCCA ACTCACCAA ATGTAAGAAA3180

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ACTAACAAAA ATATTGGTC TTCAATAATG CTAATATCT ACATTTTATG AATTTATCAA3240
CATTTAACTA GATAATTGGG CATGCTTAA TTATGCATGT ACTTATCCAT ACTAATAAAA3300
TTGACAATGC TAGTGCATAC TTATTGGTTT AGTCCTATTA TCAGGATATA ATCATCTGTG3360
AGGAGGATAT TTTAAATACT GTAAATGATA ACAGTTAATG ATATACACAT TTAGACTGAG3420
TTGCACACTG GCAGGGAGAC CAAAAACATT ACTTCCATAC TTGTGTCATG ATTCTTTTTT3480
TTTTGAGAGA GTCTCACTCT GTCGCCAGGC TGGGAGTACA GTGGCATGAT CTCGGCTCAC3540
TGCAACCTCT GCCACCCAG GTCCAAGTGA TTCTTCTGCC TCAGTCTCCC GAGTAGCTGG3600
GACTACAGGC ACCCAGGAGC ATGCCTGGCT AATTATGTA TTTTAGTAG AGACGGGTT3660
TCACCATGTT GGCCAAAGCTG GTCTCAAACCT CCTGACCTCA AGTGATCCAC CCACCTCAGC3720
CTGTCGAAGT GCTGGGATTA CAGGTGTGAG CCACTGCGCC CACCTTCTAT TTTCATCTTC3780
TTTTTAAGGA ATTAATTATT TGAATATGGC AAACATCCAC ATGGGGCCTA AAGTCAATA3840
ATGTAAAGCG ATACATTTAA AGGGCTTTAC TTCCCACCTC TTAGGTCCTT AATTCAGTCA3900
GTT

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3903

(2) INFORMATION ON SEQ ID NO. 246:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1730 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 246:

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GCATTTCTGC CATCGCCAC CGTGGCGGCA CAAGCGGCAG CCCGAGAACA CGCTGGCGGC 60
CATTCGGCAG CTAAGAATGG AGCAACAGGC GTGGAGTTGG ACATTGAGTT TACTTCGGAC 120
GGGATTCCTG TCTTAATGCA CGATAACACA GTAGATAGGA CGACTGATGG GACTGGGCGA 180
TTGTGTGATT TGACATTGA ACAAATTAGG AAGCTGAATC CTGCAGCAAA CCACAGACTC 240
AGGAATGATT TCCTGATGA AAAGATCCCT ACCCTAAGGG AAGCTGTGTC AGAGTGCCTA 300
AACCATAACC TCACAATCTT CTTTGATGTC AAAGGCCATG CACACAAGGC TACTGAGGCT 360
CTAAAGAAAA TGTATATGGA ATTTCTCTCA CTGTATAATA ATAGTGTGGT CTGTTCTTTC 420
TTGCCAGAAG TTATCTACAA GATGAGACAA ACAGATCGGG ATGTAATAAC AGCATTAACT 480
CACAGACCTT GGAGCCTAAG CCATACAGGA GATGGGAAAC CACGCTATGA TACTTTCTGG 540
AAACATTTTA TATTGTTAT GATGGACATT TTGCTCGATT GGAGCATGCA TAATATCTTG 600
TGGTACCTGT GTGGAATTC AGCTTTCCTC ATGCAAAAGG ATTTTGATC CCCGGCTAC 660
TTGAAGAAGT GGTGAGTAA AGGAATCCAG GTTGTGGTT GGACTGTAA TACCTTTGAT 720
GAAAAGAGTT ACTACGAATC CCATCTTGGT TCCAGCTATA TCACGTGACAG CATGGTAGAA 780
GACTGCGAAC CTCACCTCTA GACTTTCAGG GTGGGACGAA ACGGGTTCAG AAATGCCAG 840
GGGCCTCATA CAGGGATATC AAAATACCTT TTGTGCTAGC CCAGGCCCTG GGAATCAGG 900
TGACTCACAC AAATGCAATA GTTGGTCACT GCATTTTAC CTGAACCAAA GCTAAACCCG 960
GTGTTGCCAC CATGCACCAT GGCATGCCAG AGTTCAACAC TGTTGCTCTT GAAAATCTGG1020
GTCTGA AAAA ACGCAAGA GCCCTGCCCT TGCCCTAGCT GAGGCACACA GGGAGACCCA1080
GTGAGGATAA GCACAGATTG AATTGTACAA TTTGCAGATG CAGATGTAAA TGCATGGGAC1140
ATGCATGATA ACTCAGAGTT GACATTTTAA AACTTGGCAC ACTTATTTC AATATTGTGTA1200
CTCAGCTATG TTAACATGTA CTGTAGACAT CAAACTTTGT GCCATACTAA TAAATTTATT1260
AAAAGGAGCA CTAAGGAAAA ACTGTGTGCC AAGCATCATA TCCTAAGGCA TACGGAATTT1320
GGGGAAGCCA CCATGCAATC CAGTGAGGCT TCAGTGTACA GCAACCAAAA TGGTAGGGAG1380
GTCTTGAAGC CAATGAGGGA TTTATAGCAT CTGTAATAGA GAGCTGCAAA CCACCAGGGG1440
GCAGAGTTGC ACTTTTCCAG GCCTTTTAGG AAGCTCTGCA ACAGATGTGA TCTGATCATA1500
GGCAATTAGA ACTGGAAGAA ACTTCCAAAA AGATCTAGGG GTATGCTCAT GGTGCAAGT1560
GGGGGAAC TA AACTCTTAGG GGAGAAGAGG GGGTGACCCG CAAAAGAGAC GAGATTAGAG1620
GGAACGAGAG GGGGAAGCCG GAGAGTCCAG GAAATAAGGA GGTGAAGAAA GAAGTTGTT1680
TAAGGCGAGC TGGGGAAGTT GGAAGCCCGA AACTTGAAGG GAGGATAAAA 1730

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(2) INFORMATION ON SEQ ID NO. 247:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 3439 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 247:

CAGATTTTGC	CGGCTTTTAT	CCTTTTATTT	AACGGATTGA	AAAGAGCATA	TGCTGCCAT	60
GCAGAACATG	AAACCGAGGA	ACTGGGGAGT	GATGAAGATG	ATATTGATGA	AGATGGGCAA	120
GAATATTTGG	AGATTCTTGGC	TAAGCAGGCT	GGTGAAGATG	GAGATGATGA	AGATTGGGAA	180
GAAGATGATG	CTGAAGAGCA	TGCTCTGGAA	GGCTATTCCA	CAATCATTGA	TGATGAAGAT	240
AACCCGTGTT	ATGAGTATCA	GATATTTAAA	GCTATCTTTC	AAACTATTCA	AAATCGTAAT	300
CCTGTGTGGT	ATCAGGCACG	GACTCACGGT	CCTAATGAAG	AACAAAGAAA	ACAGTTACAG	360
GACATAGCAA	CTCTGGCTGA	TCAAAGAAGA	GCAGCCCATG	AATCCAAAAA	GATTGAGAAZ	420
CATGGAGGAT	ACAAATTCAG	TGCTCCAGTT	GTGCCAAGTT	CTTTCAATTT	TGGAGGCCCA	480
GCACCAGGGA	TGAATTGAGT	TATCTCTTTC	TTTCTGTCTG	TGTGTTTGTA	GTGAAGAGCT	540
TGTGTTTCC	CTAGTAGTGG	TTCCAGAACT	GGTTCATGTT	ATCTATTCTA	AACATAAAT	600
CAATAGATGC	ACAAAGAGAA	CAACAACCCC	AGGAGATGGG	ACCTGATCAT	GCAACCTGGC	660
ACTGGAAGAG	AAATCAGCGG	GATTTTGGGG	GTGGGGGGGA	TGGGAGGTAC	CTTAGAGGGA	720
GTATTTTCTT	TATTTTGTGA	AGAAAGTAAG	ATCCTGACTC	TGAAGCTTCA	AAGTGACACT	780
GTGGAAATCT	GAAACGAGGG	GATGTCATGA	AGGCAGCTTT	TCTTTTCTG	AGGAAAAAAT	840
AGGCATGGGC	TACAGGACTA	TTTAAATGT	CTCATTACA	GTATAAACT	CAAAGGTAGA	900
TGTAATTTTT	ACACCTATGA	GTATTGTGCC	AATTTCTGTC	TCTTCTCAC	CATTGGGTAT	960
CTATTCTTTA	TATGTAATA	AGATAAGTTC	ATCTGATAGC	CTTATTCAGT	CTTCATCATT	1020
TTCATCATTG	TTCTCATGTA	GATTATTGGA	CATTATTGTG	AGCACTACAT	AACTGATTAT	1080
AAAAATCTGT	AAATGAATTA	GCACCTTTCAT	ATTGAAACAA	GCCTCTAGC	CTATGTATAA	1140
AATAGCAAAA	TGTTTGCCTGT	TTATAAAAAA	ATGTAATGGG	GTGGGGGGCA	GGGGTAATTT	1200
CAAGTTATTA	ATTTAAAAAT	GAACTAGCAA	TTTTGTACCT	GGTGACTTTG	TGGTGCACTC	1260
ACCTCTGATA	GTGACTTTGAA	TTTCGGTATG	AAAAAGGGGT	TATGTGGTAT	TCAATTCTGC	1320
TAAAAATGAC	AACTCCCTCT	GTGTCCTGTT	TTTCTTAAAG	CTGTCAGTGT	ACAAAGTGGT	1380
ATTTGAATAC	CAGACCTTAC	TGTAAAAAAT	AAAAAAGGTG	GTATCTAGAG	CATGTAATTT	1440
GGATATAAAG	TTCTGCTCTT	AAAGAGTTGA	TCTAAGAGTA	TGGCTAAAACA	TCTATATATG	1500
CAATCTATTA	AAAGAACTTA	ATTCGGCTAT	TATGCTTTGA	TTGATTGCA	GTTTTTCTCT	1560
AATTATAACA	AAATTTTTCCT	CTATTGGCCTG	TTTTTAATCC	TGTGCCCTAGA	AGGAGTACAA	1620
AATGCACACT	TTACAAAAAT	GATATTTAAC	ACTTACCCAC	TGCTCTTTTC	CCATCTCTTC	1680
TACCGCTCTT	GTTGATCGTG	GATCTGTATC	TTGACTAGAT	AGCCCTGAAGT	ACATGGTTTC	1740
CCTCCAAAAA	CCCAATTATGA	TACCACTACA	AAAACAAGCC	AGCAAAAAAG	TACTGTAGAG	1800
AGGTTGGCTT	GCTTCCCTCT	CTTCTTAAGT	GCATGTTGAA	AAATAAGCCG	TTATTGATCT	1860
TAAACATCGG	TCAGATGAGT	CATACATTGG	GTTATTTTTT	ATATACATGT	ATACACAAGT	1920
TATTTCAAA	TGAAAGCAAC	ATCTTAATGG	ATTCAAAACT	ATTACAAGCT	GTTGTCTAAA	1980
ACAGGTGAGA	AAAAAATTTA	TAACTGTAAA	AACAAATGCA	CATATTGATA	TTAAAAATGC	2040

GTAATTAAGA AAACCCATTG TTGTTGTGTT TTTCTTGAT ACCAATAATT AAGCCACTAC2100
 TGTTGGCACT GTTTGGTTTT CTATTTTAACT ACTGAAGGAG TGAAAGTATT TCCTATATTT2160
 ATGAATTTAC TACTAAAAATC TTGGCAAAAA AAGAAAAAAA TTGTCTAACG TGTGTGGGTG2220
 AAAACTGTTA ATCAAGTGTT TCTACTCCCC CCCGAAAATC CCCTGAAAGT TGGACACCAA2280
 CTGTATACCC TAGGTTGCTT AAAGGGATT CACTATTATA TAAAGTCAAT AAAAATGAAG2340
 TAGTTGTATA TATGCAACAT TGTGTACAGA GGGGAATAA TGAATAGTAT TAAAGAAACA2400
 TTCTCGTCTT CCTTTACCTT TAATCCCCTA ATACCTAGTC TACTTTTTAA ATTTTCAGAC2460
 TTCCTGCTT TTTGAATTCA TAATTTCTAAT TTTCACATTA TTGTTAATGG AAAATCATAT2520
 CTAATAAAGG TTTTAGTTAT TCCCATGCAC AGTATGAAAA TTCTCATTTG CTGAGGTTTT2580
 GTTTCAAGAA AATGTATTGG CATGCTTTTG AGAACATGTT TTATTGCTCT CTGTGCATA2640
 TAATCCAAAC TAATCTCCGT TTACAGACTT TAACCTTGAAA TTAGACCTTA TAATTAAC2700
 ATTTAAATAG TGTTCAAATG ATAGTTTCTA ATGCATCAA TATATACCTC AGTTTTCATG2760
 ATTTCTTTA ACATTATAAT TTGGTATAGA TCAAGATCT TAACATGTAT CAGTTTCTAG2820
 ATGAGGCTGC AGGATTTTTG GAAAACTTTT TGAATGTATT TACAATATTC TCTTGAAT2880
 AGCTACATAG GGACTTGTCT TTTTTCTTTT TTACATACAG CTTTTCTTAC AGTTTTATTA2940
 CCCTGTAATT TTTTTTAGT TGTAGAAGTT AATTCTGATT TTGTGTGGAT TTCAGTATT3000

GTCTTTGTGA ATGGCACATA TTAGCATAAA TCACTTTTGT AAATGTAAGC TTTCTTTTTT3060
 TTTCTTGAAA AAGCCTTTCT ATTTATCAGT ATTAATAAAA GSAAGTTAAT CTGTTTCTCT3120
 GGAGGTAATA AAATAGTGAC ACACTGTATT AAGATAGTGA CGGCTTACT CAACCTGGA3180
 AGAGACTAGA GTATAGAGCA TGAGTGGCAA AACCACAGCC CTGGGCCAT ATGCTGCTAT3240
 TGAGTCCAG ATGTAGCCCC TGAAGCAAGC ATAAAGAAAA ATGAATTAAT AATTAAATTA3300
 ATATGGAAAG TTAATAAATG GATTACATTA GTATGACTAA ACCATGTCTT TGGCAAGAT3360
 CTAACACAAT GTCTTAAGTA TAATAGGTAG TCTCTGTTG TAAATAAAT GACTTAAAT3420
 TAAACATCA AAAAAAAA

3439

(2) INFORMATION ON SEQ ID NO. 248:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 378 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 248:

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SCSSPSCHRG HERFRIASAC LDELSCEFLF AGAGGAGAGA APGPHLPFRG SVPGDPVRIH 60
CNITESYPAV PPIWSVESDD PNLAAVLRL VDIKKGNTLL LQHLKRIISD LCKLYNLPQH 120
PDVEMLDQPL PAEQCTQEDV SSEDEDEEMP EDTEDLDHYE MKEEPPAEGK KSEDDGIGKE 180
NLAILEKIKK NQRQDYLNKA VGSVQATDR LMKELRDIYR SQSFKGGNYA VELVNDSLYD 240
WNVKLLKVDQ DSAHNDLQI LKEKEGADFI LLNFSFKDNF PFDPPFVRV SVPLSGGYVL 300
GGGAICMELL TKQGWSSAYS IESVIMQISA TLVKGKARVQ FGANKSQYSL TRAQSYKSL 360
VQIHEKNGWY TPKEDG* 378

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(2) INFORMATION ON SEQ ID NO. 249:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 281 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 249:

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AVGSAALFKD GGGGTSAAEA GAAGORLSRV NCLAYDEAIM AQDDRIQQEI AVQNPLVSR 60
LELSVLYKEY AEDDNYYQK IKDLHKKYSY IRKTRPDGNC FYRAFQFSL EALLDDSKEL 120
QRFKAVSAKS KEDLVSGQFT EFTIEDFHNT FMDLIEQVEK QTSVADLLAS FNDQSTSDYL 180
VVYLRLLTSG YLQRESKFFE HFIEGGRTVK EFCQQEVEPM CKESDHIHII ALAQALSVSI 240
QVEYMDRGEG GTTNPHIFPE GSEPKVYLLY RPHGYDILYK * 281

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(2) INFORMATION ON SEQ ID NO. 250:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 245 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 250:

DHLQPQKNLC	TCLAPGRGGQ	QGSSGLEPAL	FVEDIVVSRP	VEKVDLGLGA	LREDVRIGGA	60
ALAARVHVLHL	DGHAEGLGQR	NDVDVVALLA	HGLHLLLAEL	LDSPSTLDEV	LEELALALQV	120
RRGEQPQVDH	KVVGALVIE	GGQQVGDRL	LLHLNQVHE	RVVEILNCEF	SEALGHQVFL	180
ALGRHSLEPL	QLLAVIQQL	QVGESEPIE	TVAVRPGLAD	VRVLFVEVLD	LLLDVVVIFS	240
LLLV*						245

(2) INFORMATION ON SEQ ID NO. 251:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 294 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 251:

MLAARLVCLR	TLPSRVFHPA	FTKASPVVKN	SITKNQWLLT	PSREYATKTR	IGIRRGRTGQ	60
ELKEAALEPS	MEKIFKIDQM	GRWFFVAGGAA	VGLGALCYYG	LGLSNEIGAI	EKAVIWPQYV	120
KDRIHSTYMY	LAGSIGLTAL	SAIAISRTPV	LMNFMMRGSW	VTIGVTFEAM	VGAGMLVRSI	180
PYDQSPGPKH	LAWLLHSGVM	GAVVAPLTIL	GGPLLIRAAW	YTAGIVGGLS	TVAMCAPSEK	240
FLNMGAPLGV	GLGLVFVSSL	GSMFLPPTTR	GWCHSLLSGN	VRWISSFQHV	PSV*	294

(2) INFORMATION ON SEQ ID NO. 252:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 564 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 252:

MERELNHEKE RCDQLQAEQK GLTEVTQSLK MENEFPKKRF SDATSKAHQL EEDIVSVTHK 60
 AIEKETELDS LKDKLKKAQH EREQLECCQLK TEKDEKELYK VHLKNTIEIN TKLMSEVQTL 120
 KNLDGNKESV ITHFKEEIQR LQLCLAEKEN LQRTFLTTTS SKEDTCFLKE QLRKAEQVQ 180
 ATRQEVVFLA KELSDAVNVR DRTMADLHTA RLENEKVKKQ LADAVAEELK NAMKKDQDKT 240
 DTLEHELRRR VEDDLKRLQM AADHYKEKFK ECQRLQKQIN KLSDQSANNN NVFTKKTGNQ 300
 QKVNDASVNT DPATSASTVD VKPSPSAAEA DFDIVTKGQV CEMTKETADK TEKYNCKQL 360
 LQDEKAKCNK YADELAKMEL KWKEQVKIAE NVKLELAEVQ DNYKELKRSI ENPAERKMED 420
 GADGAFYPDE IQRPPVRVPS WGLEDNVVCV QPARNFSRPD GLEDSSEDSKE DENVPTAPDP 480
 PSQHLRGHGT GFCFDSSFDV HKKCPCLCELM FPPNYDQSKF EEHVESHVKV CPMCSEQPFP 540
 DYDQQVFERH VQTHFDQNVNL NFD*

(2) INFORMATION ON SEQ ID NO. 253:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 250 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 253:

WTGTGRGAVA IMADPDPRYP RSSIEDDFNY GSSVASATVH IRMAFLRKVY SILSLQVLLT 60
 TVTSTVFLYF ESVRTFVHES PALILLFALG SLGLIFALT NRHKYPLNLY LLFGFTLEA 120
 LTVAVVVTFY QVYIILQAFI LTTTVFFGLT VYTLQSKKDF SKFGAGLFAL LWILCLSGFL 180
 KFFFYSEIME LVLAAGALL FCGFIYDTH SLMHKLSPEE YVLAASISLYL DIINFLHLAL 240
 RFLEAVNKK*

(2) INFORMATION ON SEQ ID NO. 254:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 152 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 254:

```

EKKGETEREL SASTQTLSHL QGHLPSWPRP APTVTSASRR FIIKKNQKQS QNQNKIQKEK    60
TWGNGMRKRK GEEGRRAGLW MHNSRARGLG RKIPQRPAAC VALARHVVFQ GRLPIHPVEI   120
LVAGLLGGVK PVSDRQAGKG LGDGGCCGRER V*                                152

```

(2) INFORMATION ON SEQ ID NO. 255:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 151 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 255:

```

RHAGGGALGN LPPQPPGSGV MHPETCPSTF LASPLPHSIA PGLFLLDFFVL VLALFLIFFY    60
YESPGRRGDS GSWPGPGRQV ALEMKGKLCR GAELSLCFSF FPLLLPLHTP VAGRNLGFPE   120
SLGVPPFLPH PGGTPRAPGL FLLLSFWAV *                                151

```

(2) INFORMATION ON SEQ ID NO. 256:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 276 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 256:

GRFGQSPAGA	EEPGPRDSSA	VITQISKEEA	RGPLRGKGDQ	KSAASQKPRS	RGILHSLFCC	60
VCRDDGEALP	AHSGAPLLVE	ENGAIKPTPV	QYLLPEAKAQ	DSDKICVVID	LDETLVHSSF	120
KPVNNADFLI	PVEIDGVVHQ	VYVLKRPHVD	EFLQRMGELF	ECVLFTASLA	KYADPVADLL	180
DKWGAFRARL	FRESCVFHRG	NYVKDLSRLG	RDLRRVLILD	NSPASVVFHP	DNAVEVASWF	240
DNMSDTELHD	LLPFQEQLSR	VDDVYSVLRLQ	PRPGS*			276

(2) INFORMATION ON SEQ ID NO. 257:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 139 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 257:

MFYLAAAVSD	FYVPVSEMPE	HKIQSSGGPL	QITMKMVPKL	LSPLVKDWP	KAFIISFKLE	60
TFPAIVINRA	RKALEIYQHQ	VYVANILES	QSFVFIPTKD	SETKLLLSEE	EIEKGVEIEE	120
KIVDNLQSRH	TAFIGDRN*					139

(2) INFORMATION ON SEQ ID NO. 258:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 238 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 258:

```

PYRQGCPCGAA  GQAPGAPPGS  YYPGLPSGTP  GGPYGGAAPG  GPYQPPSS  YGAQQPGLYG  60
QGGAPPNVDP  EAYSWFQSD  SDHSGYISMK  ELKQALVNCN  WSSFNDETC  MFDRKTK  120
SGRIDVYGFS  ALWKFIQQWK  NLFOQYDRDR  SGSISYTELQ  QALSQMGYNL  PPQTQLLVS  180
RYCPRSANFA  MQLDRFIQVC  TQLQVLTEAF  REKDTAVQGN  IRLSFEDFVT  MTASRML*  238

```

(2) INFORMATION ON SEQ ID NO. 259:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 111 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 259:

```

TNICLLSGAS  PKVTNGWAQI  NFSFASHRVA  HCGKPELVRT  PVCVFLIHTN  HNKQVCTHLY  60
EPHAKTRHSQ  RSVTRVQQRN  SRFDQNRPC  LLNCQLPLKN  LQKKGHYKNS  *  111

```

(2) INFORMATION ON SEQ ID NO. 260:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 84 amino acids
 - (B) TYPE: Protein

(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 260:

FVKILKFGPL	RIILNEIYRL	TCENIFHRLS	LGLFIRKLFV	CPPVGTFGYL	ILPFQIVKAN	60
RGVFWNHLLS	HFLKSYSIVS	VNI*				84

(2) INFORMATION ON SEQ ID NO. 261:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 197 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 261:

PQTTQCVRR	GLWVNSHIHT	QGRGKHTQVQ	SSQWCRPDLL	SRGCGCP	SPEQPGQ	60
PPRLXQEGEL	CPGEETDRLG	DKTPIAGTCT	AAATAPRTGH	GDGTGREPHC	PLSVCLWFCP	120
GPAHLEPRQT	GGIEQGGPGPD	SPLARCDWKR	LMPGQHQAFC	KSQSQCAESA	STACAVAPQD	180
EVTSRRTGGFM	QTHRHC*					197

(2) INFORMATION ON SEQ ID NO. 262:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 191 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 262:

DQLGSGGHFS	LHRLPEQTEE	SSLIVAEP	SLSPSAVS	VCVLH	KPSCPR	GRDFI	LRSHST	GRAG	60
TFCTLALGLA	EGLVLPWHQ	LPVTSGQ	RAV	WTWALL	NATC	LPGLQV	GRTR	TEPQAHT	120
VWLPACPIPM	PRPRGCGCC	ACPCDGS	LV	QPV	SFLPRAE	LPFLXES	GR	CRLSWLL	180
WG									191

(2) INFORMATION ON SEQ ID NO. 263:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 245 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 263:

EKMEAFGE	GA	GWEDFF	STQT	LTFQ	SILQ	MK	NADY	FSNY	VT	EDFT	TYIN	RK	RKNN	CHGN	HI	60
EMQAMA	EMYN	RPVE	VYQYST	EPIN	TFHGI	H	QNEDE	PIRVS	YHRNI	HYNSV	VNP	NKAT	IGV			120
GLGLPS	FKPG	FAEQ	SLMKNA	IKT	SEESWIE		QQMLE	DKKRA	TDWE	ATNEAI	EEQ	VARE	SYL			180
QWL	RDQEKQA	RQVR	GPSQPR	KASAT	CSSAT		AAASS	GLEEW	TSR	S	PROQ	VQ	PRHL	STL	LSCM	240
LNWA	*															245

(2) INFORMATION ON SEQ ID NO. 264:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 221 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 264:

```
GFRPARCDPV PLPTTRSVAG LPVGRVRQLS RPLLGPDTGS VANIFKGLVI LPEMSLVIRN    60
LQRVIPIRRA PLRSKIEIVR RILGVQKFDL GIICVDNKNI QHINRIYDRD NVPTDVLSEF    120
```

```
FHEHLKAGEF PQPDFDDYN LGDIFLGVEY IFHQCKENED YNDVLTVTAT HGLCHLLGFT    180
HGTEAEWQQM FQKEKAVLDE LGRRTGTRLQ ALTRGLFEGGS *                      221
```

(2) INFORMATION ON SEQ ID NO. 265:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 109 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 265:

```
FFFLRSFVIY LCATPAPRSL HPSRVPLSEG TRPSAPSEEA PGQGLQPGPR ASAQLVQHRL    60
LLEHLLPLC LRAVCESQVQV TESVGGRRHSQ DVIVIFIFFT LMEDILHS*              109
```

(2) INFORMATION ON SEQ ID NO. 266:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 372 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 266:

MSFRKVNIII	LVLAVALLFL	VLHHNFLSL	SLLRNEVTDS	GIVGPQPIDF	VPNALRHAVD	60
GRQEEIPVVI	AASEDRLGGA	IAAINSIQHN	TRSNVIFYIV	TLNNTADHLR	SWLNSDSLKS	120
IRYKIVNFD	KLLEGKVKED	PDQGESMKPL	TFARFYLPII	VPSAKKAIYM	DDDVIVQGGI	180
LALYNTALKP	GHAAAFSEDC	DSASTKVVIR	GAGNQYNYIG	YLDYKKERIR	KLSMKASTCS	240
FNPGVFVANL	TEWKRONITN	QLEKWMKLV	EEGLYSRTLA	GSITPPILLI	VFYQHQSTID	300
PMWNVRLHGS	SAGKRYSPQF	VKAAKLLHWN	GHLPKWGRTA	SYTDVWEKWI	IPDPTGKFNL	360
IRRYTEISNI	K*					372

(2) INFORMATION ON SEQ ID NO. 267:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 73 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 267:

MCLLSQQSPA	ASSLEGAIWR	RAGTQTRALD	AILYHPQQSH	LVGSTALGLT	LPLLYPREPE	60
AGGWKDPVAG	GG*					73

(2) INFORMATION ON SEQ ID NO. 268:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 137 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 268:

VPPCPQLREL	CPGVNNQPYL	CESGHCCGET	GCCTYYYELW	WFLLWTVLI	LFSCCCAFRH	60
RRAKLRLOQQ	QRQVEINLLA	YHGACHGAGP	FPTGSLDLDR	FLSTFKPPAY	EDVVRHPTGT	120
SPPLYCGPKA	PLEVVSS					137

(2) INFORMATION ON SEQ ID NO. 269:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 309 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 269:

KHATEQEKTE	EGLGPNVKG	VTMLMLMLM	MFAVHCTWVT	SNAYSSPSV	LASYNHDGTR	60
NILDDFREAY	FWLRQNTDEH	ARVMSWWDYG	YQIAGMANRT	TLVDNNTWNN	SHIALVGKAM	120
SSNETAAYKI	MRTLDOVDYVL	VIFGGVIGYS	GDDINKFLWM	VRIAEGEHPK	DIRESDYFTP	180
QGEFRVDKAG	SPTLLNCLMY	KMSYYRFGEM	QLDFRTPPGF	DRTRNAEIGN	KDIKFKHLEE	240
AFTSEHWLVR	IYKVKAPDNR	ETLDHKPRVT	NIFPKQKYL	KKTKRKRGRY	IKNKLVFCKG	300
KKISKKTV*						309

(2) INFORMATION ON SEQ ID NO. 270:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 114 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 270:

IPEDPHIDES	KAKHQAIIMS	TSLRVSPSIH	GYHFDASRK	KAVGNIFENT	DQESLERLFR	60
NSGDKKAEER	AKIIFAIDQD	VEEKTRALMA	LKKRTKDKLF	QFLKLRKYSI	KVH*	114

(2) INFORMATION ON SEQ ID NO. 271:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 101 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 271:

```

101  QMQHFAATLQ ASLLSGLQRL ERDRDWKGTR TEQTYGKDSK QFHALCCYRG EQNAFSGDLK 60
102  TLPSTLQERID ADRAWTDVM RTKENRWLEM TFIQGHFVRP * 101

```

(2) INFORMATION ON SEQ ID NO. 272:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 21 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 272:

```

PRIPVTILNMK MVMPSGGLD *

```

21

(2) INFORMATION ON SEQ ID NO. 273:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 137 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 273:

CPPVKALIEH	EMKNGIPANR	IVLGGFSQGG	ALSLYTALTC	PHPLAGIVAL	SCWLPLHRAF	60
PQAANGSAKD	LAILQCHGEL	DPMPVVRFGA	LTAEKLRSVV	TPARVQPKTY	PGVMHSSCPQ	120
EMAAVKEFLE	KLLPPV*					137

(2) INFORMATION ON SEQ ID NO. 274:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 92 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 274:

MMWVLKLDLNT	MNVKIPPIFC	SKKKNPKNKK	TNKKPRMFFG	ITEISQTWVF	SYSLCTFFQV	60
LCFACSTDCV	ILIFIDSSLA	MQYPCLTIRC	L*			92

(2) INFORMATION ON SEQ ID NO. 275:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 76 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 275:

ETIADNALPS TEITLESPLL GSPDCLTQDV LCHSEVFIWG RSLYGDVNDS VSGLCITSHW 60
 SETPVCQAWI LHCKT* 76

(2) INFORMATION ON SEQ ID NO. 276:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 120 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 276:

GGKEKTKKIQ LNRNMIQHL QKASSISLKK ATDCASAGSE KGWAAGTAAS WVTRQQSQRL 60
 EVRLRTPPLW EHKRHHWCKL SVTWPSFLSS ISPNICAHPE ELSGNSRVRA GRGERTKRE 120

(2) INFORMATION ON SEQ ID NO. 277:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 113 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 277:

VAPFPIPTQE HRGGGEGRLS LSKSSYLHFR RKAETQSRLY INCLADRVTK THWSTCAFSS 60
 LCPSLIQTAT CQSPATLKTH GQLPGFTKLT AFLHKVKTIT ASVCGPSATT KLS 113

(2) INFORMATION ON SEQ ID NO. 278:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 86 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 278:

PYDPACLLIF SLPLPFLSLS SRSHLPGLKY FVGIAYYIIL ADEPQDNVYT HTHTYTHTKS 60
 QLLKSGLGIR LLCPVKNSCT EVIVT* 86

(2) INFORMATION ON SEQ ID NO. 279:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 70 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 279:

NSFKVVKKLA TTWSLSIKRK QGKQTHSLDQ KKLDQVHWNQ SVTTQVTMTS VQEFFTGHRH 60
 LIPSPLFNS* 80

(2) INFORMATION ON SEQ ID NO. 280:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 594 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 280:

VSEKCRIDTE	ILPSLFMRCT	TDLNRKDKFP	AITHLKFLAR	DMSEQVLLCA	SSQTSSIVEC	60
WSLRKEGLPV	NNIFOQISPV	VGDKQPTILK	WRILSATNDL	DRVSAVALPK	LPISLTNTDL	120
KVASDTQFYP	GLGLALAFHD	GSVHIVHRLS	LQTMVVFYSS	AAPRPVDEPA	MKRPRTAGPA	180
VHLKAMQLSW	TSLALVGIDS	HGKLSVLRLS	PSMGHPLEVG	LALRHLLFLL	EYCMVTGYDW	240
WDILLHVQPS	MVQSLVEKLH	EEYTRQTAAL	QQVLSTRILA	MKASLCKLSP	CTVTRVCDYH	300
TKLFLIAISS	TLKSLLRPHF	LNTPKSPGD	RLTEICTKIT	DVIDKVMIN	LKTEEFVLDM	360
NTLQALQQLL	QWVGDFVLYL	LASLPNQSSL	LRPGHSFLRD	GTSLGMLREL	MVVIRIWGLL	420
KPSCLPVYTA	TSDTQDSMSL	LFRLLTKLWI	CCRDEGPASE	PDEALVDECC	LLPSQLLIPS	480
LDWLFPASDGL	VSRLQPKQPL	RLQFGRAPTL	PGSAATLQLD	GLARAPGQPK	IDHLRRLHLG	540
ACPTTECKAC	TRCGCVTMLK	SPNRTTAVKQ	WEQRWIKNCL	CGGLWWRVPL	SYP*	594

(2) INFORMATION ON SEQ ID NO. 281:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 293 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 281:

LRGRTRHQSP	HRQFLIQRCS	HCFTAVVLLG	DLSMVTQPHL	VQALHSSVVG	APRCSLRRWS	60
ILGWPGALAR	PSSCRVAALP	GSVGARPNCR	RRGCLGCRRL	TRPSLAGSQS	RLGISSWLGS	120
RQHSSTSASS	GSLAGPSSRQ	QIQSLVSRRK	SROMLSWVSE	VAVYTGRQLC	FRRPQMRMTT	180
INSRSMPEV	PSRKLWPGGL	SREFWLGRLA	SRYSKSPH	CKSCCSACSV	FMSSNTSSVL	240
RLIMTISMST	SVILVQISVS	RSPGLLSGVL	RKWGRSSDFR	VELMAMRKSL	VW*	293

(2) INFORMATION ON SEQ ID NO. 282:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 173 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 282:

```

TPALRARSIR DRCARAPCPH GGQQRRRRL NAEGAEGARG GGSSYSEMAE TVADTRRLIT   60
KPQNLNDAYG PPSNFLEIDV SNPQTVGVGR GRETTYEIRV KTNLPFIKFK ESTVRRRYSY  120
FEWLIRSELER ESKVVVPPLP GKAFIRQFLL EEMMEYLMIT LLRKENKGWS SL*      173

```

(2) INFORMATION ON SEQ ID NO. 283:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 107 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 283:

```

NYLGRFQPQW FNDNKTTHKG TSNSLIKLLS HLFHRMMRFF LFTVSHQGGK NPPTSCLFFG   60
LMPGISIHCL FKRPQKQVD KALAQELGLP VVVPGLPCWG VPKSV*                   107

```

(2) INFORMATION ON SEQ ID NO. 284:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 105 amino acids
 - (B) TYPE: Protein

- (C) STRAND: individual
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 284:

```

MGNFFFFEPG TCYVAQAGLE LLNSSDPLTS ASQIAETGT HHCTWLKTIF LKNKSTALHL 60
YLLVSLQFKH TINDYNILFK AGRSGSWLQL EQFITSGYLR ARKIQ 105

```

(2) INFORMATION ON SEQ ID NO. 285:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 119 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 285:

```

TGMGGGSGCR ELLCPCKGAE TPVELRKSDG IYRVLGKPWL CLHHGERPWA GSPPSCRSVR 60
LDADGGSDQL ASVSLRHEAA FSSGFQSHSG LPMADRVAKV RNGKCIAYVL PSPTKQIT* 119

```

(2) INFORMATION ON SEQ ID NO. 286:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 110 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 286:

YANQSSSLRF KIKYKLLCFS THSGSIVPEP DCYFFILNII FPHLICLPPI HRHLEKEMGG 60
CLLSLSLCFV PVRRLAASVA RWALEFPWVR QVAGGDRERL RGKWWHLLL* 110

(2) INFORMATION ON SEQ ID NO. 287:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 75 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 287:

SQLLGRLRQE NHLNSGGRC SELRSCHCTP AWATRVKLRL KKKKKEMFFI FFMLSIALF 60
HHGQQVIFHNV DFPK* 75

(2) INFORMATION ON SEQ ID NO. 288:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 67 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 288:

RRGFLHVGQA GLEFLTSGDP PASATQSAGI TGISHRERPI LLFIYFLRWS LALFRDLRPL 60
QPSPLQF 67

(2) INFORMATION ON SEQ ID NO. 289:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 85 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 289:

STRPRERRNR	SVDECQLINV	KXRHLVCLX	CFCLYXQPD	VSXEYKXWGL	LPQXLFXIS	60
EKKNDRXXGX	IXRXARFXST	NXNX*				85

(2) INFORMATION ON SEQ ID NO. 290:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 78 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 290:

MSXXDTXWCV	XAVFAFTXNP	TVFHXNINXG	XFYPXLSSXL	VKKKKMIGXX	XFXGKPPXXQ	60
ALXKIXSWXX	LTSLPXX*					78

(2) INFORMATION ON SEQ ID NO. 291:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 310 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 291:

RAASGRSGSS	VRMSAPRSRP	ASMRWCPAPR	RACTTSTRWT	GPPCATSTSS	ARATRTGPSC	60
RSAGRARSAS	YPPGDVDEIP	DWVHQLVIQK	LVEHRVIPEG	FVNSAVINDY	QPGGCIIVSHV	120
DPIHIFERFI	VSVSFFSDSA	LCFGCKFQFK	PIRVSEPVLS	LPVRRGSVTV	LSGYAADEIT	180
HCIRPQDIKE	RRAVIILRKT	RLDAPRLETK	SLSSSVLPFS	YASDRLSGNN	BDPALKEPKRS	240
HRKADPDAAH	RPRILEMDKE	ENRRSVLLFT	HRRRGSFSE	NYWRKSYESS	EDCSEAAGSP	300
ARKVKMRRH*						310

(2) INFORMATION ON SEQ ID NO. 292:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 192 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 292:

SCLPEDDDCS	ALLDVLRPYA	VSDFISSIST	EHSHASPAHR	QGKHWFRRPN	RLELELAEEA	60
QRRVAKEGHG	HDGALEDVDG	VHVGHDAAAG	LUVVDDRAVD	EALGDDAVLH	QLLDHQLMHP	120
VRDLVDVARR	VRGAGPAPA	SAAGPRTCSP	RRRSTCCAGG	GPPECARCTG	PSRRGTPPHR	180
CGPRSWSTHP	D*					192

(2) INFORMATION ON SEQ ID NO. 293:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 479 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 293:

MGRCCFYTAG	TLSSLLLVTS	VTLLVARVFQ	KAVDQSIIEK	IVLRNGTEAF	DSWEKPPPLPV	60
YTQFYFNV	NPEEILRG	PRVEEVGPY	YRELNRKANI	QFGDNGTTIS	AVSNKAYVFE	120
RDQSVGDPKI	DLIRTLNIPV	LTVIEWSQVH	FLREIIEAML	KAYQOKLFVT	HTVDELLWGY	180
KDEILSLIHV	FRPDISPYFG	LFYEKNGTND	GDYVFLTGED	SYLNFTKIVE	WNGKTSLDWW	240
ITDKCNMNG	TDGDSFHPLI	TKDEVLYVFP	SDFCRSVYIT	FSDYESVQGL	PAFRYKVP	300
ILANTSDNAG	FCIPEGNCLG	SGVLNVISICK	NGAPIIMSFP	HFYQADERFV	SAIEGMHPNQ	360
EDHETFDIN	PLTGIIILKAA	KRFQINIYVK	KLDDFVETGD	IRTMVFPVMY	LNESVHIDKE	420
TASRLKSMIN	TTLIITNIPY	IIMALGVFFG	LVFTWLACKG	QGSMDDEGTAD	ERAPLIRT*	479

(2) INFORMATION ON SEQ ID NO. 294:

- (i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 267 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 294:

AFLPSPTVAA	QAAAREHAGG	HSAAKNGATG	VELDIEFTSD	GIPVLMHDNT	VDRTTDGTGR	60
LCDLTFFQIR	KLNPAAHRL	RNDFPDEKIP	TLREAVAACL	NHNLTIFFDV	KGHAHKATEA	120
LKKMYMEFPQ	LYNNSVVCSE	LPEVIYKMRQ	TDRDVITALT	HRPWSLSHTG	DGKPRYDTFW	180
KHFIFVMMDI	LLDWSMHNL	WYLCGISAFI	MQKDFVSPAY	LKKWSAKGIQ	VVGWTVNTFD	240
EKSYYESHG	SSYITDSMVE	DCEPHF*				267

(2) INFORMATION ON SEQ ID NO. 295:

- (i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 166 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 295:

QILPAFILLF	NGLKRAYACH	AEHETEELGS	DEDDIDEDGQ	EYLEILAKQA	GEDGDDEDWE	60
EDDAEETALE	GYSTIIDDED	NPVDEYQIFK	AIFQTIONRN	PVWYQALTHG	LNEEQRKQLQ	120
DIATLADQRR	AAHESKMIEK	HGGYKFSAPV	VPSSFNFGGP	APGMN*		166

QILPAFILLF
EDDAEETALE
DIATLADQRR

WO 99/46375

PCT/DE99/00722

Claims

1. A nucleic acid sequence that codes a gene product or a part thereof, comprising

- a) a nucleic acid sequence, selected from the group Seq. ID No. 3, 4, 6-8, 12, 16-19, 21, 23, 24, 26-33, 35, 37, 41-44, 46, 47, 49, 51, 53, 54, 58-64 and 217-247,
- b) an allelic variation of the nucleic acid sequences named under a)

or

- c) a nucleic acid sequence that is complementary to the nucleic acid sequences named under a) or b).

2. A nucleic acid sequence according to one of the sequences Seq. ID No. 3, 4, 6-8, 12, 16-19, 21, 23, 24, 26-33, 35, 37, 41-44, 46, 47, 49, 51, 53, 54, 58-64 and 217-247, or a complementary or allelic variant thereof.

3. Nucleic acid sequence Seq. ID No. 2-4, 6-10, 12-14, 16-19, 21, 23, 24, 26-33, 35-37, 39, 41-44, 46, 47, 49, 51-55, 58-64 and 217-247, characterized in that it is expressed elevated in normal prostate tissue.

4. BAC, PAC and Cosmid clones containing functional genes and their chromosomal localization according to sequences Seq. ID No. 3, 4, 6-8, 12, 16-19, 21, 23, 24, 26-33, 35, 37, 41-44, 46, 47, 49, 51, 53, 54, 58-64 and 217-247 for use as a vehicle for gene transfer.

5. A nucleic acid sequence according to claims 1 to 4, wherein it has 90% homology to a human nucleic acid sequence.

6. A nucleic acid sequence according to claims 1 to 4, wherein it has 95% homology to a human nucleic acid sequence.

7. A nucleic acid sequence comprising a portion of the nucleic acid sequences named in claims 1 to 6, in such a sufficient amount that they hybridize with the sequences according to claims 1 to 6.

8. A nucleic acid sequence according to claims 1 to 7, wherein the size of the fragment has a length of at least 50 to 2500 bp.

9. A nucleic acid sequence according to claims 1 to 7, wherein the size of the fragment has a length of at least 150 to 2000 bp.

10. A nucleic acid sequence according to one of claims 1 to 9, which codes at least one partial sequence of a bioactive polypeptide.

11. An expression cassette, comprising a nucleic acid fragment or a sequence according to one of claims 1 to 9, together with at least one control or regulatory sequence.

12. An expression cassette, comprising a nucleic acid fragment or a sequence according to claim 11, in which the control or regulatory sequence is a suitable promoter.

13. An expression cassette according to one of claims 11 and 12, wherein the DNA sequences located on the cassette code a fusion protein, which comprises a known protein and a bioactive polypeptide fragment.

14. Use of nucleic acid sequences according to claims 1 to 10 for producing full-length genes.

15. A DNA fragment, comprising a gene that can be obtained from the use according to claim 14.

16. Host cell, containing as the heterologous part of its expressible genetic information a nucleic acid fragment according to one of claims 1 to 10.

17. Host cell according to claim 16, wherein it is a prokaryotic or eukaryotic cell system.

18. Host cell according to one of claims 16 or 17, wherein the prokaryotic cell system is E. coli and the eukaryotic cell system is an animal, human or yeast cell system.

19. A process for producing a polypeptide or a fragment, wherein the host cells according to claims 16 to 18 are cultivated.

20. An antibody which is directed against a polypeptide or a fragment which by the nucleic acids of sequences Seq. ID No. 3, 4, 6-8, 12, 16-19, 21, 23, 24, 26-33, 35, 37, 41-44, 46, 47, 49, 51, 53, 54, 58-64 and 217-247, which can be obtained according to claim 19.

21. An antibody according to claim 20, wherein it is monoclonal.

22. A protein according to claim 20, wherein it originates from a phage display.

23. Polypeptide partial sequences according to sequences Seq. ID No. 66-71, 73-75, 82, 83, 90-93, 97-105, 109, 111-114,

116-124, 128-137, 139-149, 152, 154-165, 168-173, 183-195, 214-216 and up to Seq. ID No. 248-295.

24. Polypeptide partial sequences according to claim 22, with at least 80% homology to these sequences.

25. Polypeptide partial sequences according to claim 22, with at least 90% homology to these sequences.

26. Use of polypeptide partial sequences according to sequences Seq. ID No. 66-71, 73-75, 82, 83, 90-93, 97-105, 109, 111-114, 116-124, 128-137, 139-149, 152, 154-165, 168-173, 183-195, 214-216 and up to Seq. ID No. 248-295 as tools for finding active agents against prostate cancer.

27. Use of nucleic acid sequences according to sequences Seq. ID No. 3, 4, 6-8, 12, 16-19, 21, 23, 24, 26-33, 35, 37, 41-44, 46, 47, 49, 51, 53, 54, 58-64 and 217-247 for expression of polypeptides that can be used as tools for finding active agents against prostate cancer.

28. Use of nucleic acid sequences Seq. ID No. 3, 4, 6-8, 12, 16-19, 21, 23, 24, 26-33, 35, 37, 41-44, 46, 47, 49, 51, 53, 54, 58-64 and 217-247 in sense or antisense form.

29. Use of polypeptide partial sequences Seq. ID No. 66-71, 73-75, 82, 83, 90-93, 97-105, 109, 111-114, 116-124, 128-137, 139-149, 152, 154-165, 168-173, 183-195, 214-216 and up to Seq. ID No. 248-295 as pharmaceutical agents in gene therapy for treatment of prostate cancer.

30. Use of polypeptide partial sequences Seq. ID No. 66-71, 73-75, 82, 83, 90-93, 97-105, 109, 111-114, 116-124, 128-137, 139-149, 152, 154-165, 168-173, 183-195, 214-216 and up to Seq.

ID No. 248-295 to produce a pharmaceutical agent for treatment of prostate cancer.

31. Pharmaceutical agent, containing at least one polypeptide partial sequence Seq. ID No. 66-71, 73-75, 82, 83, 90-93, 97-105, 109, 111-114, 116-124, 128-137, 139-149, 152, 154-165, 168-173, 183-195, 214-216 and up to Seq. ID No. 248-295.

32. A nucleic acid sequence according to claims 1 to 10, wherein it is a genomic sequence.

33. A nucleic acid sequence according to claims 1 to 10, wherein it is an mRNA sequence.

34. Genomic genes, their promoters, enhancers, silencers, exon structure, intron structure and their splice variants, obtainable from cDNAs of sequences Seq. ID No. 3, 4, 6-8, 12, 16-19, 21, 23, 24, 26-33, 35, 37, 41-44, 46, 47, 49, 51, 53, 54, 58-64 and 217-247.

35. Use of the genomic genes according to claim 33, together with suitable regulatory elements.

36. Use according to claim 34, wherein the regulatory element is a suitable promoter and/or enhancer.

37. A nucleic acid sequence according to claims 1 to 7, wherein the size of the fragment has a length of at least 400 to 1900 bp.

Systematic Gene Search in the Incyte LifeSeq Database

Normal tissue
-50,000 individual ESTs

Tumor tissue
-50,000 individual ESTs

Priority list

High

Prostate
Breast
Ovary
Bladder
Uterus

Iterative assembling
with
increasing mismatch

Low

-8,000 contigs
+
-25,000 singletons

-8,000 contigs
+
-25,000 singletons

Comparison of databases

normal tissue-
specific
(expected: 100-500)

nonspecifically
expressed genes

tumor tissue-
specific
(expected: 100-500)

Genes of Interest

Figure 1

REPLACEMENT PAGE (RULE 26)

Systematische Gen-Suche in der Incyte LifeSeq Datenbank

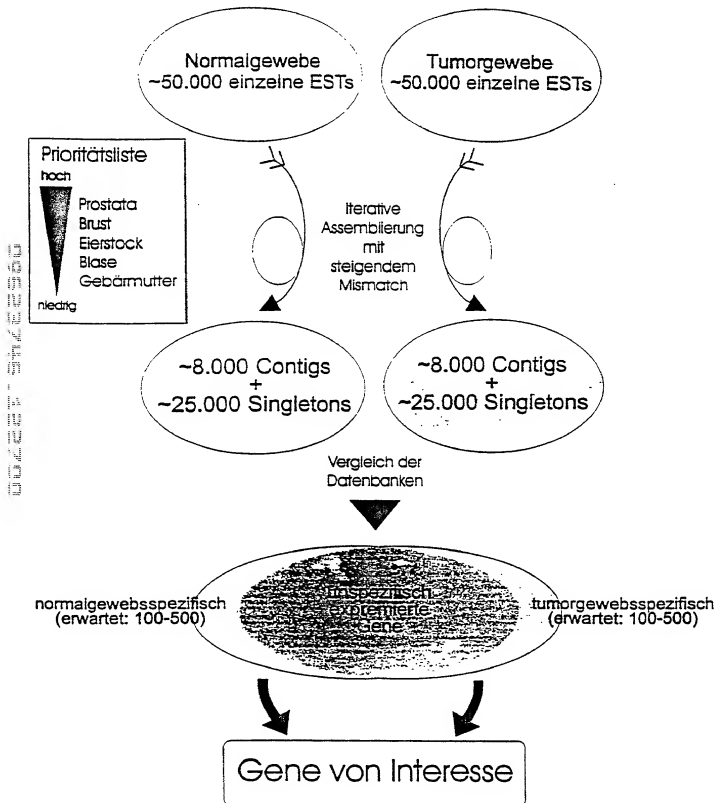


Fig. 1

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Principle of EST Assembly

-50,000 ESTs per tissue

Assembly at 0% mismatch
with GAP4 (Staden)

Contigs

Singletons

Contigs increasing in
number and lengthIterative assembly with
increasing mismatch
(1%, 2%, 4%)

5000-6000 contigs

-25,000 other
singletons-30,000 consensus-
sequences per tissue

Figure 2a

REPLACEMENT PAGE (RULE 26)

Prinzip der EST-Assemblierung

~50.000 ESTs pro Gewebe

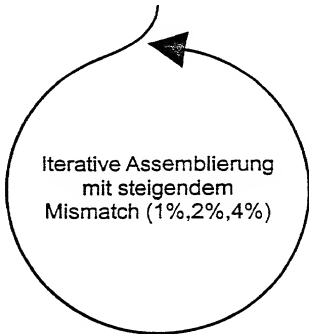
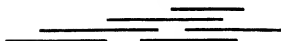


Assemblierung bei 0% Mismatch
mit GAP4 (Staden)



Contigs

Singletons



In Anzahl und Länge zunehmende Contigs

5000-6000 Contigs ~25.000 übrige Singletons



~30.000 Konsensus-
sequenzen pro Gewebe

Fig. 2a

3/10

-50,000 ESTs of a tissue (e.g.: uterus tumor)

GAP4 Assembly 1st Round:
minimum initial match: 20
maximum pads per read: 8
maximum percent mismatch: 0

GAP4 Database 1
Contigs 1
Singletons 1

unassembled
ESTs

GAP4 Assembly 2nd Round:
minimum initial match: 20
maximum pads per read: 8
maximum percent mismatch: 1

GAP4 Database 2
Contigs 2
Singletons 2

unassembled
ESTs

GAP4 Assembly 3rd Round:
minimum initial match: 20
maximum pads per read: 8
maximum percent mismatch: 2

GAP4 Database 3:
Contigs 3
Singletons 3

unassembled
ESTs

Figure 2b1

REPLACEMENT PAGE (RULE 26)

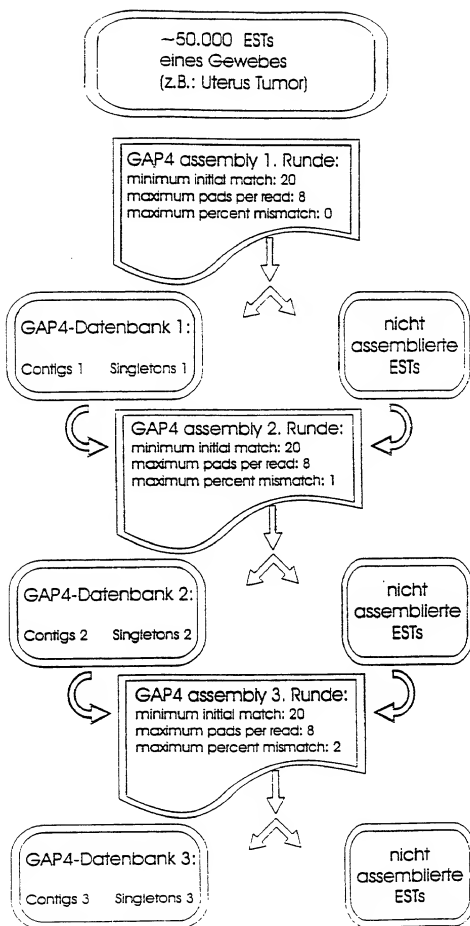


Fig. 2b1

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GAP4 Database 3:
Contigs 3
Singletons 3

unassembled
ESTs

Consensus 3

GAP4 Assembly 4th Round:
minimum initial match: 20
maximum pads per read: 8
maximum percent mismatch: 2

GAP4 Database 4:
Contigs 4
Singletons 4

unassembled
ESTs

Consensus 4

GAP4 Assembly 5th Round:
minimum initial match: 20
maximum pads per read: 8
maximum percent mismatch: 4

GAP4 Database 5:
Contigs 5
Singletons 5

unassembled
ESTs 5

Consensus 5

Singletons 5

Figure 2b2

REPLACEMENT PAGE (RULE 26)

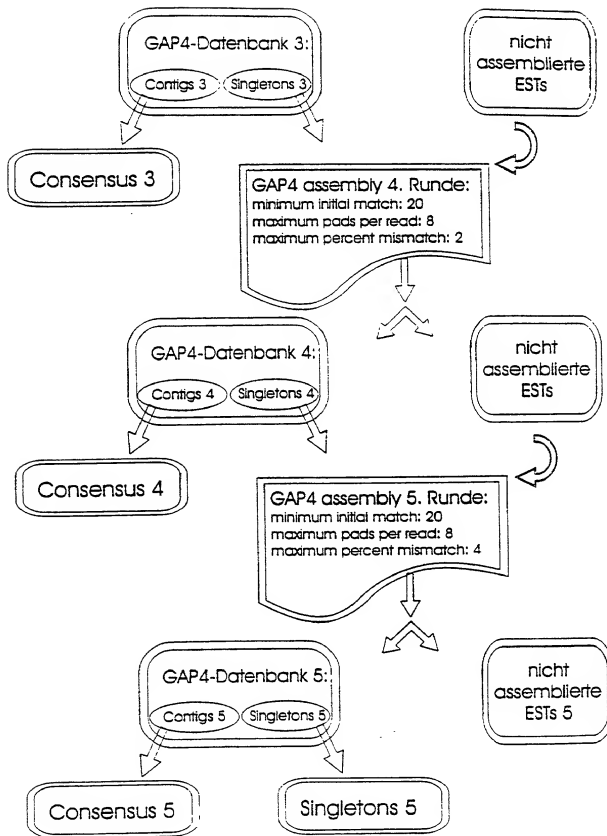


Fig. 2b2

09/623746

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Consensus 3

Singletons 5

Consensus 4

unassembled
ESTs 5

Consensus 5

GAP4 Assembly 6th Round:
minimum initial match: 20
maximum pads per read: 8
maximum percent mismatch: 4

Assembled database
of a specific tissue
(e.g.: uterus tumor)

Figure 2b3

REPLACEMENT PAGE (RULE 26)

5/10

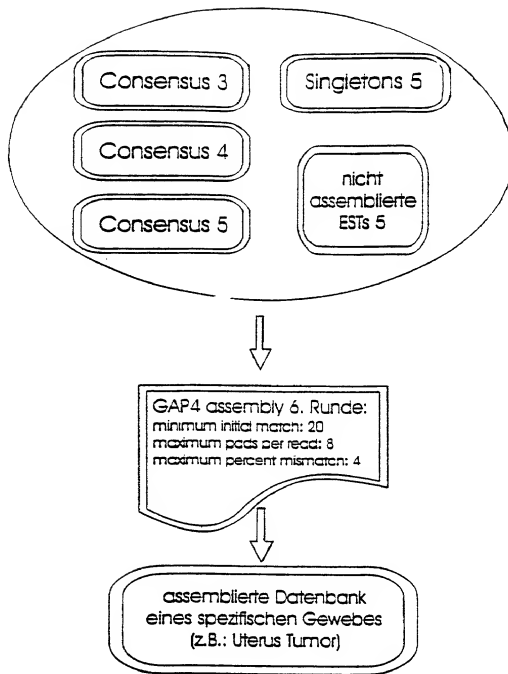


Fig. 2b3

6/10

Assembled database
of a specific tissue
(e.g.: uterus tumor)

Consensus 6

Read-in as singletons

Database
of a specific tissue
(e.g.: uterus tumor)

Database of a second
specific tissue
(e.g.: normal uterus)

GAP4 Assembly
minimum initial match: 20
maximum pads per read: 8
maximum percent mismatch: 4

Tumor tissue-
specific ESTs

Non-tissue-
specific ESTs

Normal tissue-
specific ESTs

Fig. 2b4

REPLACEMENT PAGE (RULE 26)

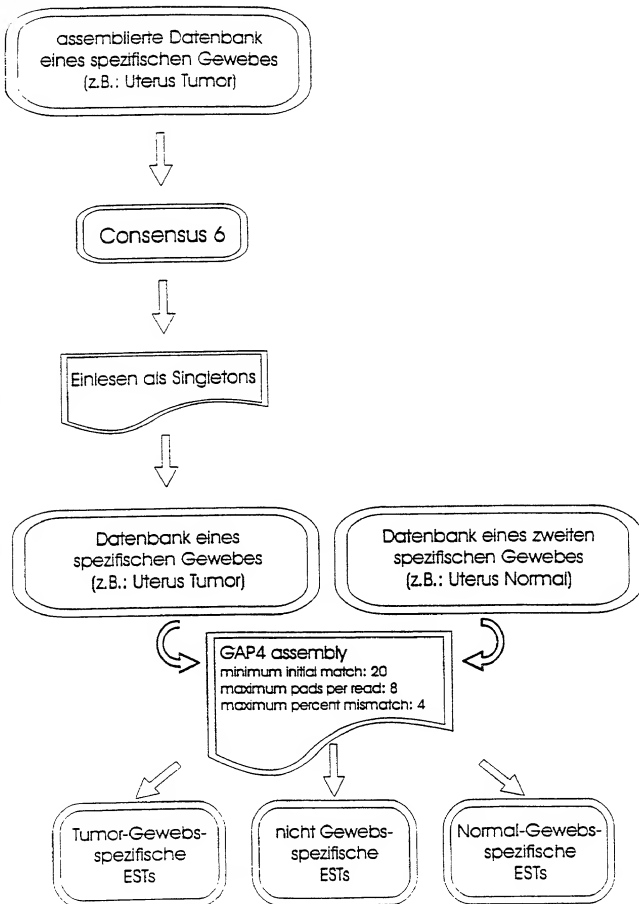


Fig. 2b4

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In silico subtraction of gene expression in various tissues

~30,000 consensus sequences
normal tissue

~30,000 consensus sequences
tumor tissue

Assembling at 4% mismatch

Normal tissue
Specific genes

Cancer tissue
Specific genes

Genes expressed in both tissues

Figure 3

REPLACEMENT PAGE (RULE 26)

In silico Subtraktion der Genexpression in verschiedenen Geweben

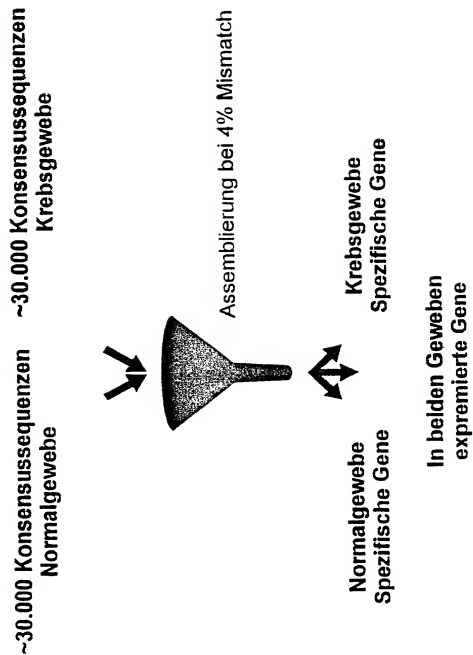


Fig. 3

Genes of interest

Determination of tissue-specific expression
via electronic Northern (INCYTE LifeSeq and
public EST databases)

Candidate genes for tumor suppressors or
tumor activators

Figure 4a

REPLACEMENT PAGE (RULE 26)

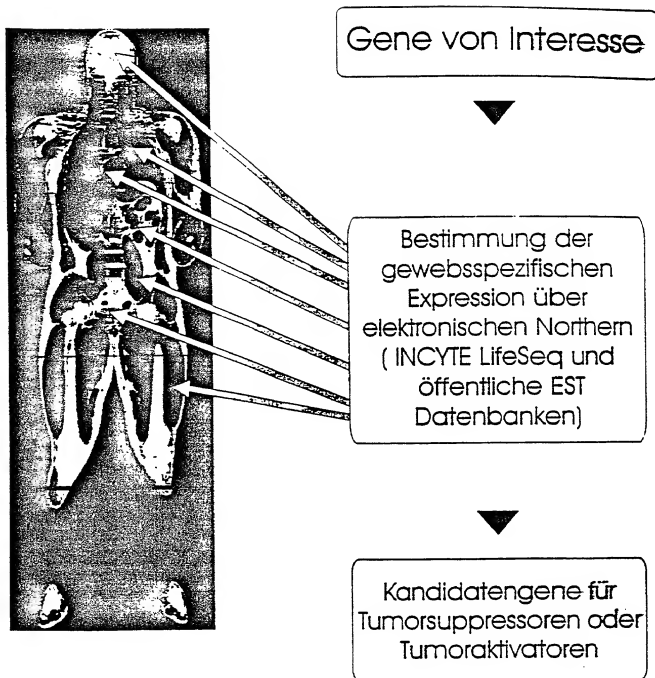


Fig. 4a

9/10

Partial cDNA sequence
 e.g. EST or contig
 S

...GCCTCAAGTTATC...

WHILE $C_i > C_{i-1}$

Electronic Northern Blot

Fisher's Exact Test IF H_0 EXIT

Automatic Lengthening

Consensus sequence C

...ATGTCCTAGCCTCAAGTTATCAGATGCAA...

Figure 4b

REPLACEMENT PAGE (RULE 26)

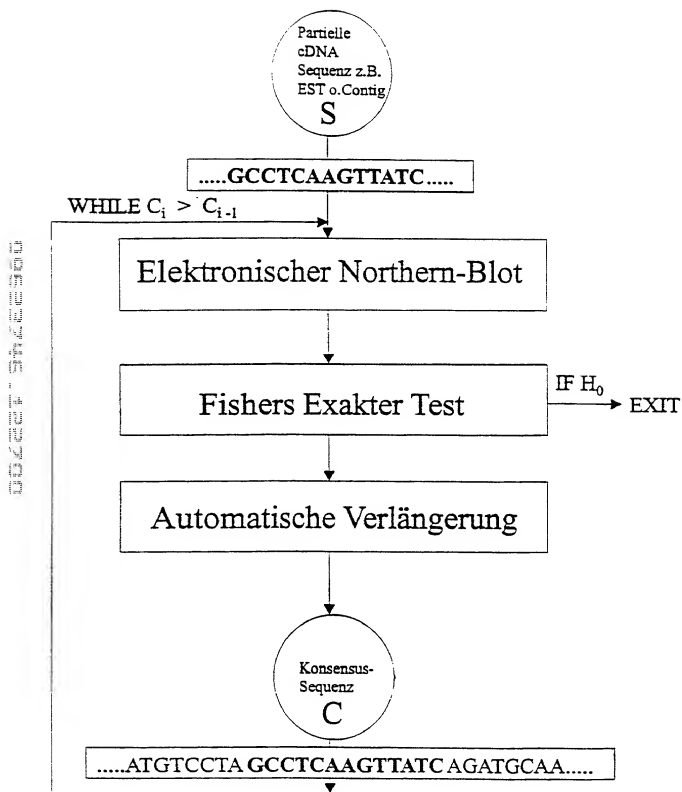


Fig. 4b

10/10

Isolation of genomic BAC and PAC clones

Chromosomal clone localization via FISH

Hybridization signal

Sequencing of clones that are located in regions that have chromosomal deletions in prostate and breast cancer leads to identification of candidate genes

Exon Intron

Confirmation of candidate genes by screening of mutations and/or deletions in cancer tissues

Figure 5

REPLACEMENT PAGE (RULE 26)

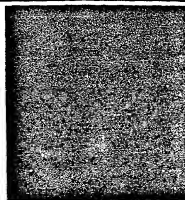
Isolieren von genomischen BAC und PAC Klonen



Chromosomale Klon-Lokalisation über FISH



Hybridisierungssignal



Sequenzierung von Klonen, die in Regionen lokalisiert sind, die chromosomale Deletionen in Prostata- und Brustkrebs aufweisen, führt zur Identifizierung von Kandidatengenen



Bestätigung der Kandidatengene durch Screening von Mutationen und/oder Deletionen in Krebsgeweben

Fig. 5

Systematic Gene Search in the Incyte LifeSeq Database

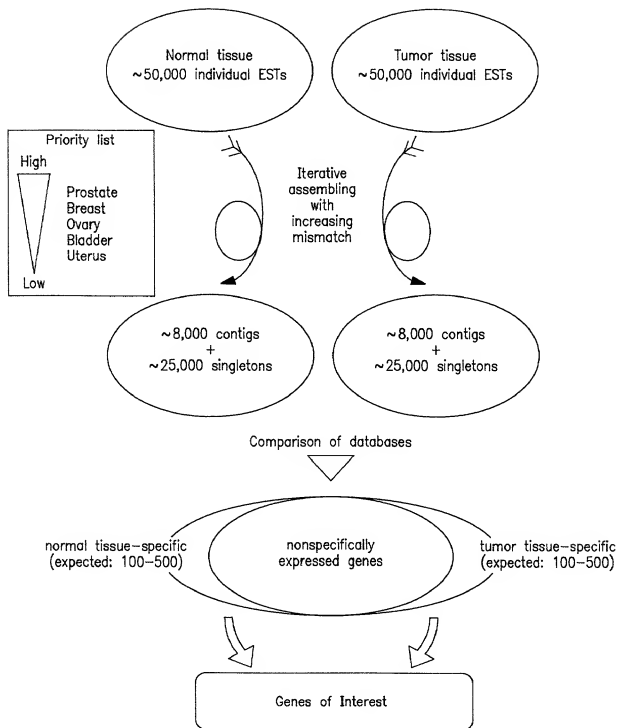
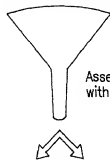


FIG. 1

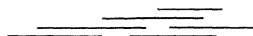
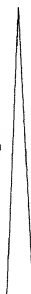
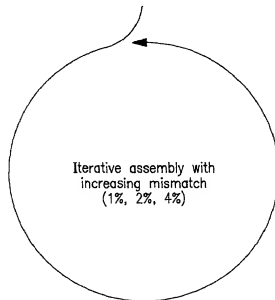
Principle of EST Assembly

~50,000 ESTs per tissue

Assembly at 0% mismatch
with GAP4 (Staden)

Contigs

Singletons

Contigs increasing in
number and lengthIterative assembly with
increasing mismatch
(1%, 2%, 4%)

5000-6000 Contigs ~25,000 other singletons

~30,000 consensus-
sequences per tissue

FIG. 2a

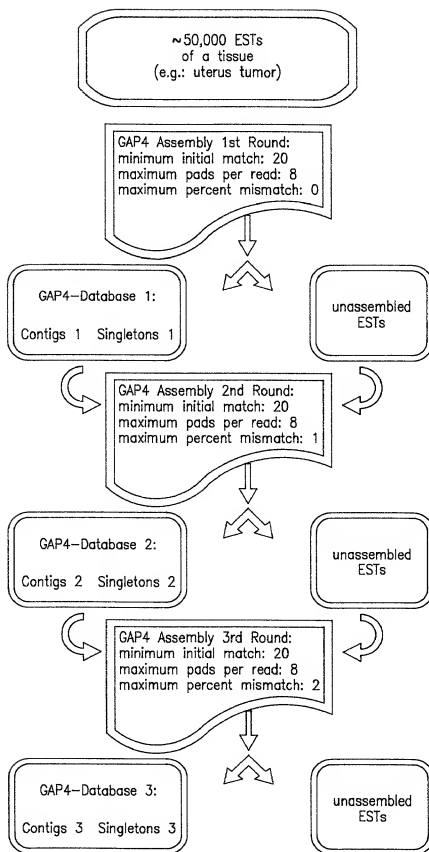


FIG. 2b-1

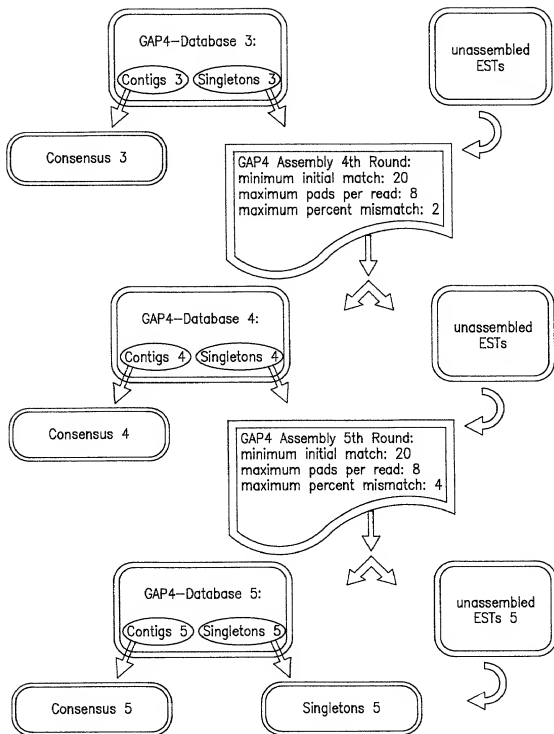


FIG. 2b-2

09/623746

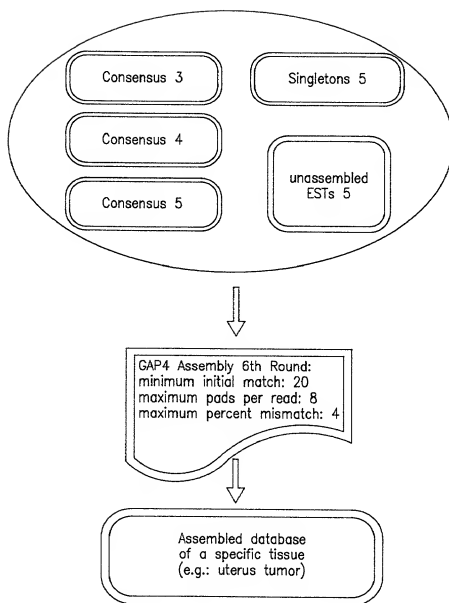


FIG. 2b-3

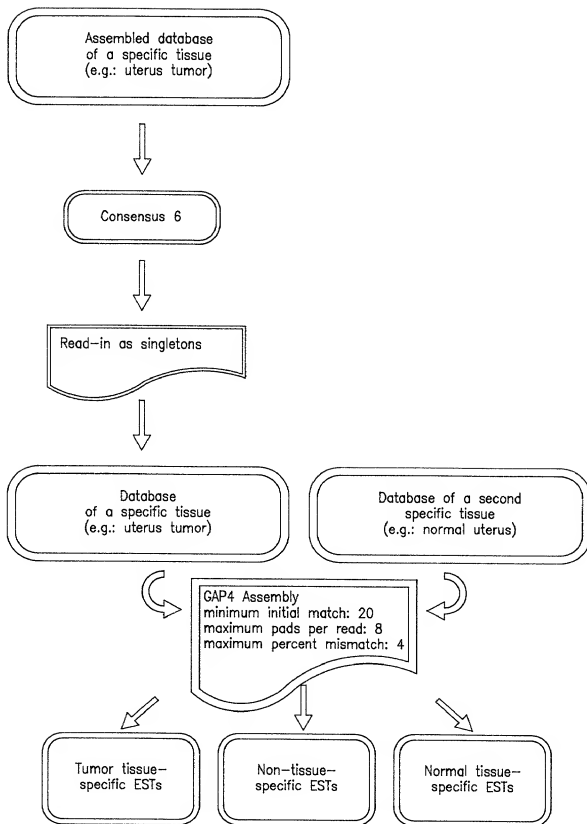
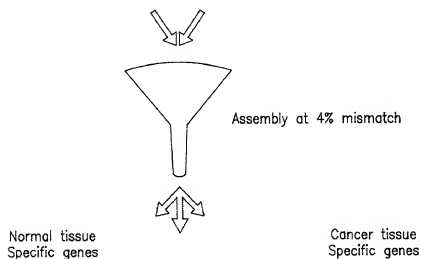


FIG. 2b-4

In silico subtraction of gene expression in various tissues

~30,000 consensus sequences
normal tissue

~30,000 consensus sequences
cancer tissue



Genes expressed in both tissues

FIG. 3

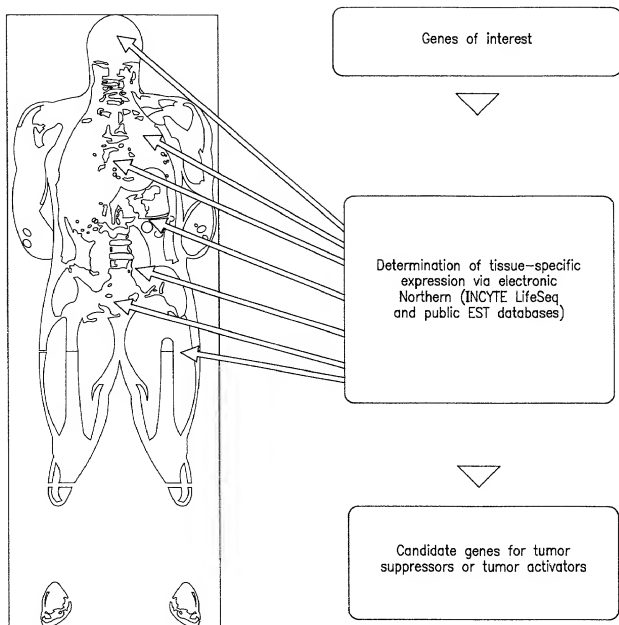


FIG. 4a

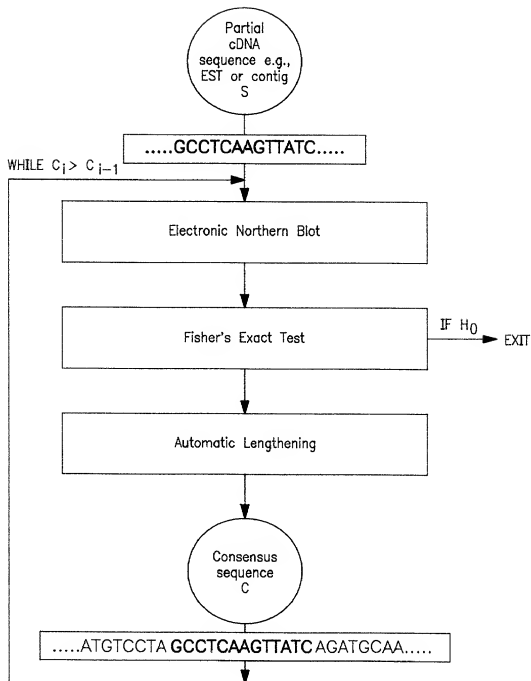


FIG. 4b

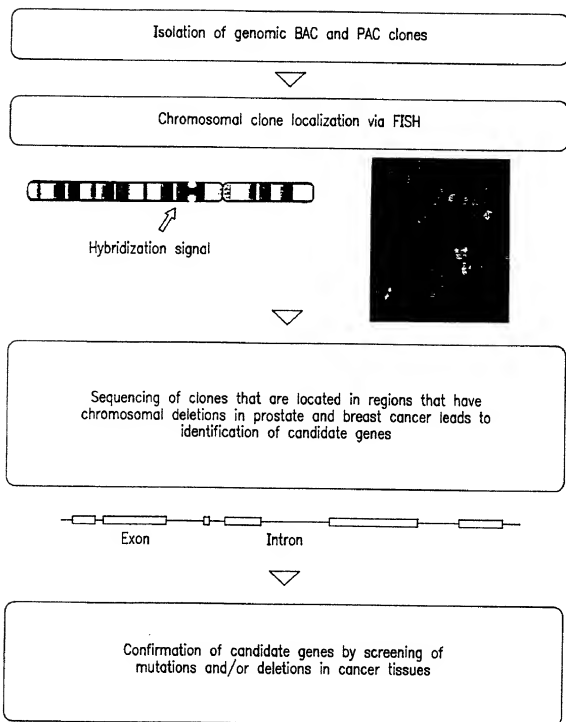


FIG. 5

Attorney Docket Number

SCH 1761

DECLARATION FOR PATENT APPLICATION

As a below named inventor, I hereby declare that

My residence post office address and citizenship are as stated below next to my name

I believe I am the original, first and sole inventor (if only one name is listed below) or an original, first and joint inventor (if plural names are listed below) of the subject matter which is claimed and for which a patent is sought on the invention entitled

HUMAN NUCLEIC ACID SEQUENCES FROM PROSTATE TISSUE

the specification of which

☐ is attached hereto

☒ was filed on 9 MARCH 1999 as United States Application Number or PCT International Application Number PCT/DE99/00722 and (if applicable) was amended on _____

I hereby authorize our attorneys to insert the serial number assigned to this application

I hereby state that I have reviewed and understand the contents of the above-identified specification, including the claims, as amended by any amendment referred to above

I acknowledge the duty to disclose information which is material to patentability as defined in 37 CFR §1.56

I hereby claim foreign priority benefits under 35 U.S.C. §119(a)-(d) or §365(b) of any foreign application(s) for patent or inventor's certificate or §365(a) of any PCT International application which designated at least one country other than the United States listed below and have also identified below, by checking the box, any foreign application for patent or inventor's certificate, or PCT international application having a filing date before that of the application on which priority is claimed

PRIOR FOREIGN/PCT APPLICATION(S) AND ANY PRIORITY CLAIMS UNDER 35 USC §119			
APPLICATION NO.	COUNTRY	DAY/MONTH/YEAR FILED	PRIORITY CLAIMED
198 11 194.0	GERMANY	10/03/98	YES

I hereby claim the benefit under 35 U.S.C. §119(e) of any United States provisional application(s) listed below

PROVISIONAL APPLICATION(S) UNDER 35 U.S.C. §119(e)	
APPLICATION NUMBER	FILING DATE

I hereby claim the benefit under 35 U.S.C. §120 of any United States application, or §365(c) of any PCT International application designating the United States listed below and, insofar as the subject matter of each of the claims of this application is not disclosed in the prior United States or PCT International application in the manner provided by the first paragraph of 35 U.S.C. §112

I acknowledge the duty to disclose information which is material to patentability as defined in 37 CFR §1.56 which became available between the filing date of the prior application and the national or PCT International filing date of this application

PRIOR U.S./PCT INTERNATIONAL APPLICATION(S) DESIGNATED FOR BENEFIT UNDER 37 U.S.C. §120		
APPLICATION NO	FILING DATE	STATUS — PATENTED, PENDING, ABANDONED

I hereby appoint the following attorney(s) and/or agent(s) to prosecute this application and to transact all business in the Patent and Trademark Office connected herewith: I. William Millen (19,544); John L. White (17,745); Anthony J. Zeilano (27,969); Alan E. J. Branigan (20,565); John R. Moses (24,983); Harry B. Shubin (32,004); Brian P. Heaney (32,542); Richard J. Traverso (30,595); John A. Sopp (33,103); Richard M. Lebovitz (37,067); John H. Thomas (33,480); Catherine M. Joyce (40,668); Nancy J. Axeirod (44,014); James T. Moore (35,619); James E. Ruland (40,921) and Jennifer J. Branigan (37,432)

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Declaration for Patent Application (Continued)

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true, and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patent issued thereon

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□ Additional joint inventors are named on separately numbered sheets attached hereto.

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